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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on:

7, 2005, 12:36:09 ; Search time 42 Seconds (without alignments) 1184.383 Million cell updates/sec July

Title:

US-10-618-173-2 2712 1 MMSRDTKTESQQSQGTSSSSASTSSCSEILPTSAEKRAKR Perfect score: Sequence:

517

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283416 283416 segs, 96216763 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR 79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:* 4 3 2 1 Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	י ב	Ča2+/calmodulin-de	Ca2+/calmodulin-de	protein kinase RAD	protein kinase Cds	myosin-light-chain	Ca2+/calmodulin-de	probable protein k	Ca2+/calmodulin-de	protein kinase (EC	Ca2+/calmodulin-de	Ca2+/calmodulin-de	Ca2+/calmodulin-de	ribosomal protein	phosphorylase kina	ribosomal protein	Ca2+/calmodulin-de	probable serine/th	serine/threonine-s	ribosomal protein	hypothetical prote	Ca2+/calmodulin-de	calmodulin-depende	Ca2+/calmodulin-de	serine/threonine-s	serine/threonine-s	serine/threonine-s	serine-t	probable protein k
SUMMARIES	ID	439	S50193	S57347	A39616	S58882	A40811	S17656	T43420	T37321	A45472	TVRTC4	152637	A53036	A53300	851600	151901	JN0323	T10449	JC1446	B32571	T18445	JU0270	B44412	D44412	S59941	A56009	T52633	T38226	T08777
	DB	-	-1	Н	-	N	-	Н	N	~	~	-	~	-	~	7	~	7	7	-	н	7	-	7	~	~	н	7	~	7
	Length	513	374	370	821	460	301	469	445	348	524	474	502	473	735	260	735	414	504	512	724	608	516	509	530	473	511	512	504	542
di	Query Match	1 (2	Т	Н	21.2	20.8	20.7	19.9	19.8	19.8	19.7	1.9.7	19.7	19.6	18.7	18.7	18.6	18.5	18.5	18.5	18.4	18.4	18.2	18.2	18.2	18.2	18.1	18.0	18.0	17.9
	Score	62	593.5	591.5	575.5	563.5	560.5	539.5	538	537	535	534.5	534.5	531	507.5	909	503.5	501.5	501.5	501	498.5	498	494.5	493.5	493.5	492.5	490	488	487	484.5
	Result No.		7	m	4	S	9	7	80	თ	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29

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protein kinase C (protein K07A9.2 (i	Ca2+/calmodulin-de	Ca2+/calmodulin-de	Ca2+/calmodulin-de	Ca2+/calmodulin-de	protein kinase C (Ca2+/calmodulin-de	probable Ca-calmod	probable calcium d	probable serine/th	calcium dependent	ribosomal protein	SNF-related kinase	calcium-dependent	GIN4 protein - yea
148719 B88640	B46619	S43845	A31908	JC5636	A53215	A34366	T40939	F85059	T07788	T51156	A32571	B90100	S71776	859359
7	Н	Н	Н	~	H	H	7	~	7	~	н	7	Н	0
918 310	518	518	527	556	915	533	580	520	512	503	752	472	490	1142
17.8	17.7	17.7	17.7	17.7	17.7	17.6	17.6	17.5	17.4	17.3	17.3	17.3	17.3	17.3
	ī.	3.5	9.5	5.5	479	8.5	8.5	473.5	71.5	70.5	2.0	469	469	468
484	479	47	47	47		4	4	4	4	4	4			

ALIGNMENTS

 RESULT 1 843941 protein kinase DUN1 (EC 2.7.1) - yeast (Saccharomyces cerevisiae) N'Alternate names: protein D2370; protein YDL101c
C;Species: Saccharcomyces cerevisiae C;Date: 13-Jan-1995 #sequence revision 13-Jan-1995 #text_change 09-Jul-2004 C;Accession: S43941; S67643; S67418; S72106 R;Zhou, Z; Blledge, S.J.
A.Title: DINI encodes a protein kinase that controls the DNA damage response in yeast. A;Reference number: S43941; MUD:94084787; PMID:8261511 A;Accession: S43941 A;Molecule type: DNA
A; Residues: 1-513 <zho> A; Cross-references: 1.513 <zho> A; Cross-references: UNIPROT: P39009; EMBL: L25548; NID: g435616; PIDN: AAA16124.1; PID: g43561 A; Rallesta, J.P.G.; Remacha, M.; Soler-Mira, A.; Jimenez, A.; Garcia-Cantalejo, J.M.; Bos submitted to the Protein Sequence Database, July 1996 A; Reference number: S67629 A; Accession: S6743 A; Accession: S6743</zho></zho>
A; Residues: 1.513 < BAL> A; Residues: 1.513 < BAL> A; Cross-references: EMBL: Z74149; NID: 91431139; PIDN: CAA98668.1; PID: 91431140; GSPDB: GN000(A; Experimental source: strain \$288C A; Experimental source: strain \$288C R; Boskovic, J.; Salz, J.E.; Soler-Mira, A.; Garcia-Cantalejo, J.; Revuelta, J.L.; Jiminez submitted to the EMBL Data Library, February 1996 A; Reference number: \$67406 A; Accession: \$67418
 A.Molecule type: DNA A,Rolecule type: DNA A,Rosidues: 1-513 -260S> A,Cross-references: EMBL:X95644; NID:g1199535; PIDN:CAA64912.1; PID:g1199548 A,Cross-references: EMBL:X95644; NID:g1199535; PIDN:CAA64912.1; PID:g1199548 R,Saiz, J.E.; Buitrago, M.J.; Garcia, R.; Revuelta, J.L.; del Rey, F. Yeast 12, 1077-1084, 1996 A,Saiz, 1077-1084, 1996 A,Title: The sequence agenere a 20.3 kb DNA fragment from the left arm of Saccharomyces cerevi A,Reference number: S72094; MUD:97051597; PMID:8896274 A,Rocession: S72104
A; Yetatus: nutleic acid sequence not snown; translation not snown A; Wolecule type: DNA A; Wolecule type: DNA A; Roserices: EMBL:X95644; NID:g1199535; PIDN:CAA64912.1; PID:g1199548 A; Note: the nucleotide sequence was submitted to the EMBL Data Library; February 1996 C; Genetics: DDUNI; MIPS:YDL101c A; Cross-references: MIPS:YDL101c; SGD:S0002259 A; Map position: 4L
C.Function: A.Description: catalyzes the formation of peptidyl-serine-phosphate or peptidyl-threonine A.Description: catalyzes the formation of peptidyl-serine-phosphate or peptidyl-threonine C.Supwords: ATP, protein kinase DUNI; kinase interaction domain homology; protein kinase homology of KH> F.58-128/Domain: kinase interaction domain homology of KH> F.198-480/Domain: protein kinase homology of KH> F.206-214/Region: protein kinase ATP-binding motif

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187 425

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C, Keywords: ATP; autophosphorylation; calmodulin binding; phosphoprotein; phosphotransfers F;18-276/Domain: protein kinase homology <KIN> F;26-34/Region: protein kinase ATP-binding motif F;293-299/Region: autoinhibitory F;233-299/Region: calmodulin binding F;317/Binding site: phosphate (Thr) (covalent) (by autophosphorylation) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ca2+/Calmodulin-dependent protein kinase (EC 2.7.1.123) I - human
NyAlternate names: CaMKI
NyAlternate names: CaMKI
C;Species: Hone sapiens (man)
C;Space: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
C;Accession: S57347
R;Haribabu, B.; Hook, S.S.; Selbert, M.A.; Goldstein, E.G.; Tomhave, E.D.; Edelman, A.M.; A;Title: Human calcium-calmodulin dependent protein kinase I: cDNA cloning, domain struct
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A, Cross-treferences: UNIPROT:Q14012, EMBL:L41816; NID:g790789; PIDN:AAA99458.1; PID:g79075
A, Cross-treferences: UNIPROT:Q14012, EMBL:L41816; NID:g790789; PIDN:AAA99458.1; PID:g79075
C, Genetics:
A, Generics: GDB:GAAR.
A, Cross-treferences: GDB:642249
C, Superfamily: Ca2+/calmodulin-dependent protein kinase homology
C, Superfamily: ATP; autophosphorylatrion; calmodulin binding; phosphoprotein; phosphotransfe); P;18-276/Domain: protein kinase homology & KIND.
F;26-34/Region: protein kinase ATP-binding motif
F;293-299/Region: autocinhibitory
F;26-34/Region: calmodulin binding
F;302-314/Region: calmodulin binding
F;302-314/Region: calmodulin binding
F;307-314/Region: Calmodulin binding
F;307-314/Region: Calmodulin binding
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                                                                                                                                                                                                                                                                                                                                                                                                                    246 EILKKLDHPCIIKIENFFDSEDFYYIVLELMEGGELFDRVVNSTRLREPIAKLYFYQMLL 305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                188 EVL---AQKPYSKAVDCWSIGVIAYILLCGYPPFYDEN-DAKLFEQILKAEYEFDSPYWD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AVQYLHENGVIHRDLKPENVLLSSTSEECCIKITDFGQSKILGETSLMRTLCGTPTYLAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       366 EVLNTAGTTGYSSAVDCWSLGVILFVCLCGYPPFSEQNSNIPLKNQIAEGKYTYIAAAWR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NVSEQAFDLVKNLLVVDPEQRLTTKQALEHPWLQDDSMKHTVERLMYGVDHTMPPPIKKN
                                                                                                                                                                                                                                                                                                           186 KDFIDKYIMSRPIGSGACGEVKLAFQKSVCKKVAVKIISKRKFKMNTSSNEHPISVDTEI
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                                                                                                                                                                                                                                                        19;
                                                                                                                                                                                                 DB 1; Length 374;
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                                                                                                                                                                                               21.9%; Score 593.5; DB 1; Length 39.9%; Pred. No. 2.9e-20; ive 62; Mismatches 106; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Reference number: S57347; MUID:95369239; PMID:7641687
A;Accession: S57347
A;Status: preliminary; nucleic acid sequence not shown
A;Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      21.8%; Score 591.5; DB 1; ilarity 39.9%; Pred. No. 3.5e-20; Conservative 61; Mismatches 107;
                                                                                                                                                                                                                        Best Local Similarity 39.9
Matches 124; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             486 IIRKRGHEWDQ 496
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 298 FAKSK---WKQ 305
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Matches 124;
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C;Species: Rattus norregicus (Norway rat)
C;Species: Rattus norregicus (Norway rat)
C;Species: Rattus norregicus (Norway rat)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
C;Accession: S50193; A46082; A46038
R;Cho, F.S.; Phillips, K.S.; Bogucki, B.; Weaver, T.E.
Biochim: Biophys. Acta 1224, 156-160, 1994
A;Title: Characterization of a rat cDNA clone encoding calcium/calmodulin-dependent prot A;Reference number: S50193; MUD:95035115; PMID:7948038
A;Reference number: S50193; MUD:95035115; PMID:7948038
A;Reference number: S50193
A;Reference number: S50193
A;References: UNIPROT: Q63450; EMBL:L26288; NID:948038
A;References: UNIPROT: Q63450; EMBL:L26288; NID:9439613; PIDN:AAA66944.1; PID:94396
B;Picciotto, M.R.; Czernik, A.J.; Nairn, A.C.
J; Biol. Chem. 269, 26512-26521, 1993
A;Title: Calcium/calmodulin-dependent protein kinase I. cDNA cloning and identification A;Reference number: A49682
A;Reference number: A49682
A;Residues: preliminary
A;Rolccule type: mRNA
A;Residues: 1-111, G', 113-117, R', 119-308; R', 310-322, 'HQPG', 327, T', 329, 'TDS' <PIC>
A;Cross-references: GB.L24907; NID:9406112; PIDN:AAA19670.1; PID:9406113
B;Rochizuki, H.; Ito, T:; Hidaka, H.
J; Biol. Chem. 269, 9143-9147, 1993
A;Title: Purification and characterization of Ca2+/calmodulin-dependent protein kinase V
A;Reference number: A46038; MUID:9322082; PMID:9386178
A;Arcesesion: A66038; MUID:9322082; PMID:9386178
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C;Superfamily: Ca2+/calmodulin-dependent protein kinase I; protein kinase homology
                                                              12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          113 VK-KDYILKNGDRIVFGKSCSFLFKYASSSSTDIENDDEKVSSESRSYKNDDEVFKKPQI
                                                                                                                                                                                                                                                                                                                                     -----YPKDFIDKYIMSRPIGSGACGEVKLAFQKSVCKKVAVKII
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VDCWSLGVILFVCLCGYPPFSEQNSNIPLKNQIAEGKYTYIAAAWRNVSEQAFDLVKNLL
                                                                                                               GRDKKCDYTFDIPVLNQTDRYKTYSKRHFRIFQELGHGHSRVANIEDLSGNGTFVNKEII
                                                              Gaps
                                                           90;
  Length 513;
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  ; Score 621; DB 1; Length 51;
; Pred. No. 2.2e-21;
73; Mismatches 152; Indels
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Ca2+/calmodulin-dependent protein kinase (EC 2.7.1.123) I
                                                                                                                                                                                                                        GKGRILPLINNAEIALSLPINKVFVF----SDLSVDDQTI--
     22.9%;
                            32.1%;
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A;Residues: 12-36,'T' <MOC>
A;Experimental source: cerebrum
                                                      Matches 149; Conservative
                               Best Local Similarity
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A; Status: prelimina
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qq	: : : ::: :: ::::	Best Local Similarity 28.6%; Pred. No. 4e-19; Matches 148; Conservative 81; Mismatches 166; Indels 123; Gaps 12;
λŏ	306 AVQYLHENGVIHRDLKPENVLLSSTSEECCIKITDFGQSKILGETSLMRTLCGTPTYLAP 365	Qy 10 SQQSQGTSSSSSAPQSYSQSSSSGTLSSLDTVPVQDL-ASIPEDPEIDEDIPQ 63
Ор	128 AVKYLHDLGIVHRDLKPENLLYYSLDEDSKIMISDFGLSKMEDPGSVLSTACGTPGYVAP 187	bb 5 TQPTQQSTQATQRFLIEKFSQEQIGENIVCRVICTTGQIPIRDLSADISQVLKEKRSIKK 64
& a	366 EVLNTAGTTGYSSAVDCWSLGVILFVCLCGYPPFSEQNSNIPLKNOIAEGKYTYIAAAWR 425	Qy 64 PWGRLWALGKGFLNHDCLHEEYVFGRDKKCDYTFDIPVLNQTDRYKTYSKRHFRIFQELG 123
oy Op	426 NVSEQAFDLVKNILVVDPEQRLTTKQALEHPWLQDDSMKHTVERLMYGVDHTMPFPIKKN 485 11	Qy 124 HGHSRVANIEDLSGNGTFVNKEIIGKGRTLPLTNNAEI
ó	486 IIRKRGHEWDQ 496	Qy 162ALSLPTNKVFVFSDLSVDDQTIYPKDFIDK 191
ДQ	298 FAKSKWKQ 305	Db . 153 QCLEQNKVDRIRSNLKNTSKIASPGLTSSTASSMVANKTGIFKDFSIIDEV 203
RESULT 4 A39616 protein k. NiAlternal C; Species C; Date: 33 C; Date: 33 C; Date: 34 A; Title: 6 A; Title: 6 A; Recessine A; Rolecul A; Referen A; Rolecul A; Referen A; Rolecul A; Residue A; Residue A; Rossiue	RESULT 4 A39516 Protein Kinase RAD53 (EC 2.7.1.) - yeast (Saccharomyces cerevisiae) By Ctein Kinase RAD53 (EC 2.7.1.) - yeast (Saccharomyces cerevisiae) CSpecies: Saccharomyces cerevisiae CSpecies: Saccharomyces cerevisiae CSPECIES: Saccharomyces cerevisiae CARCESSION: A39516; SESIGH, 559446; S1331 CARCESSION: D. 13, 2910, 131, 2910, 2011 ARCESSION: A39516; SESIGH, MUD53117267; PMED189989 ARCESSION: A39516; MUD507; PS2216; GB:MS5623; MID;G172656; PIDN:AAA35070.1; PID;G172657 ARCESSION: A39516; MUD507; A39516; MUD507; MU	Oy 139 YIMSEDIGGAGGROUGHOUS CHECKNOTHS CREPGENTS SINGH IN THE INCL. 21 Db 22 DHCLIKIENFUGGAGGROUGH IN THE INCL. I

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Best Local Similarity 38.73
Matches 116; Conservative
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C;Function:
C;Cuperfamily:
A,Title: S-phase specific activation of Cds1 kinase defines a subpathway of the checkpoi
A,Reference number: 226084; MUID:98119835; PMID:9450932
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N.Alternate names: MLCK-A
C.Species: Dictyostelium discoideum
C.Spate: 10-Apr-1992 #sequence_revision 21-Jan-1997 #text_change 09-Jul-2004
C.Accession: A40811; A37125
R.Tan, J.L.; Spudich, J.A.
J. Biol. Chem. 266, 16044-16049, 1991
A.Title: Characterization and bacterial expression of the Dictyostelium myosin light A; Ritle: Characterization and bacterial expression of the Dictyostelium myosin light A; Recession: A40811; MUID:91340753; PMID:1651931
A; Molecule type: mRNA
A; Residues: 1-310 r TAN>
A; Kross-references: UNIPROT:P25323; GB:M64176; NID:g1498249; PIDN:AAB06337.1; PID:g14
R; Tan, J.L.; Spudich, J.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         13;
                                                                                                         A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-202,'1',204-237,'F',239-460 <LIN>
A;Residues: B:EMBL:AJ222869; NID:g2689196; PIDN:CAAl1019.1; PID:g2689197
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            196 RPIGSGACGEVKLAFQKSVCKKVAVKIISKRKFKMNTSSNEHPISVDTEIELLKKLDHPC 255
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291 THRDIKPENILITN---DFHLKISDFGLAKVIHGTGTFLETFCGTMGYLAPEVLKSKNVN 347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IHRDLKPENVLLSSTSEECCIKITDFGQSKIL-GETSLMRTLCGTPTYLAPEVLNTAGTT 374
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                142 VNKEIIGKGRTLPLTNNAE--IALSLPTNKVFVFSDLSV----DDQTIYPKDFIDKYIMS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     87 FGRDKKCDYTFDIPVLNQTDRYKTYSKRHFRIFOELGHGH-----SRVANIEDLSGNGTF
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                                                                                                                                                                                                                                                                                                 Gene: SPBC18B5.11c; cds1
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A;Gene: SPBC18B5.1
A;Map position: 3
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J. Biol. Chem. 265, 13818-13824, 1990

A;Title: Dictyostelium myosin light chain kinase. Purification and characterization.

A;Reference number: A37125; MUID:90337997; PMID:2380188

A;Accession: A37125

A;Molecule type: protein

A;Residues: 9-12,'I',14-19;163-167,'S',169-179;192-198 <TA2>
C;Genetics:
A;Gene: mikA

C;Function:
A;Gene: mikA

C;Gene: 
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A; Residues: 315-469 <SIK>
A; Cross-references: 315-469 <SIK>
A; Cross-references: GB: MI6206; NID: g200360; PIDN: AAA39933.1; PID: g387512
A; Sikela, J.M.; Law, M.L.; Kao, F.
Genomics 4, 21-27, 1989
A; Title: Chromosomal localization of the human gene for brain Ca2+/calmodulin-dependent I
A; Reference number: 149571; MUID: 89122027; PMID: 2536634
A; Recession: 149571
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A;Molecule type: mRNA
A;Molecule type: mRNA
A;Rolecule type: mRNA
A;Rolecule type: mRNA
A;Rolecule type: mRNA
A;Rolecule type: mRNA
B;Cross-references: UNIPROT:P08414; EMBL:X58995; NID:g50366; PIDN:CAA41741.1; PID:g50367
R;Sikela, J.M.; Hahn, W.E.
A;Sikela, J.M.; Hahn, W.E.
A;Title: Screening an expression library with a ligand probe: isolation and sequence of a A;Reference number: A29878; MUID:87204263; PMID:3033675
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C;Species: Nus musculus (house mouse)
C;Date: 10-Sep-1999 #sequence revision 10-Sep-1999 #text_change 09-Jul-2004
C;Accession: S17656; A29878; I49571
R;Jones, D.A.; Glod, J.; Wilson-Shaw, D.; Hahn, W.E.; Sikela, J.M.
FEBS Lett. 289, 105-109, 1991
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Superfamily: Ca2+/calmodulin-dependent protein kinase I; protein kinase homology; Keywords: ATP; autophosphorylation; calmodulin binding; phosphoprotein; phosphotransfer
                                                                                                                                                                      62 VSVGRSNTCNY----QLLQFTASYK-----HFRVYSVLIDDDMDPLVYCEDQSSNGTFLN 112
                                                                                                                                                                                                                                                                                                                                                                                                                            219
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RDLKLENILIASSSDTIFRIILTDFGVARCMQKGKRLSTFVGTPEYTAPBIQRLKGRSQV 339
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                                                                                                                                  143
                                                                                                                                                                                                                                                     144 KEIIGKGRTLPLTNNAEIALSLPTNKVFVFSDLSVDDQTIYPKDFIDKY-----IMSRP 197
                                                                                                                                                                                                                                                                                 220 KVNMEYNSETQFFIFEEMVTGGDLFSYLTKLGTVPEVTTLFIMFQILQGLKYLHEQNIH 279
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RDLKPENVLLSSTSEECC-IKITDFGQSKILGETSLMRTLCGTPTYLAPEVLNTAG---- 372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KKLDHPCIIKIENFFDSEDFYYIVLELMEGGELFDRVVNSTRLREPIAKLYFYQMLLAVQ 308
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                  84
                                                                        61
                                                                                                                                                                                                                                                                                                                                                                                                    20 EKYDFRDVLGTGAFSKVFLAESKSDAGOMYAVKCIDKKALKGKEE-----SLENEIKVL
                                                                                                                                  85 YVFGRDKKCDYTFDIPVLNQTDRYKTYSKRHFRIFQEL-GHGHSRVANIEDLSGNGTFVN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DKYIMSRPIGSGACGEVKLAFOKSVCKKV-AVKIISKRKFKMNTSSNEHPISVDTEIEIL
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                  SQSSSSGTLSSLDTVPVQDLASIPEDPEIDEDIPQPWGRLWALGKG----FLNHDCLHEE
                                                                        10 SRSESTQILCELSQIDESTM-----DPQYTED--DVLARLFVFSSSSPQTVLNVK-KYED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ----TIGYSSAVDCWSLGVILFVCLCGYPPFSEQNSNIPLKNQIAEGKYTYIAAAWRNVS
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                                                                                                                                                                                                                                                                                                                                                                   IGSGACGEVKLAFQKSVCKKVAVKIISKRFKMNTSSNEHPISVDTEIEILKKLDHPCII
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19.8%; Score 537; DB 2; Length 34:
Best Local Similarity 39.2%; Pred. No. 9.4e-18;
Matches 118; Conservative 60; Mismatches 105; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             429 EQAFDLVKNLLVVDPEQRLTTKQALEHPWLQDDSMKHT 466
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A;Status: preliminary; translated from GB/EWBL/DDBJ
A;Molecule type: mRNA
A;Molecule type: mSNA
B;Molecule typ
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A; Reference number: 222503
A; Accession: T43420
A; Accession: T43420
A; Residues: translated from GB/EMBL/DDBJ
A; Residues: 1-445 < LNA
A; Residues: UNIPROT: Q10292; EMBL: Z71478; PIDN: CAA96101.1
A; Experimental source: strain 972h(-)
B; Devlin, K.; Churcher, C.M.; Barrell, B.G.; Rajandream, M.A.; Wood, V.
Submitted to the EMBL Data Library, August 1997
A; Reference number: Z2137
A; Accession: T37688
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Molecule type: DNA
A; Residues: 1-445 < CDEV>
A; Residues: 1-445 < CDEV>
A; Cross-references: EMBL: Z96596; PIDN: CAB11196.1; GSPDB: GN00066; SPDB: SPAC14C4.03
A; Experimental source: strain 972h-; cosmid c14C4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            probable protein kinase (EC 2.7.1.-) mekl - fission yeast (Schizosaccharomyces pombe) C.Species: Schizosaccharomyces pombe C.Sapecies: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 16-Aug-2004 R;Lyne, M.H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  15;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           174 SDLSVDDQTIYPKDFIDK------YIMSRPIGSGACGEVKLAFQKSVCKKVAVKIIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     15 SSVTASTENLVPDYWIDGSNRDPLGDFFEVESELGRGATSIVYRCKQKGTQKPYALKVLK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     21;
                                                                                                                                                                                                                                                                                                                                                                                                 DB 1; Length 469;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                        Query Match
19.9%; Score 539.5; DB 1;
Best Local Similarity 39.8%; Pred. No. 9.6e-18;
Matches 117; Conservative 53; Mismatches 103;
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A;Introns: 53/1; 231/2
C;Superfamily: protein kinase homology
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Best Local Similarity 31.9
Matches 146; Conservative
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us-10-618-173-2.rpr

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Ca2+/Calmodulin-dependent protein kinase (EC 2.7.1.123) IV - rat
NyAlternate names: Ca2+/Calmodulin-dependent protein kinase Gr
NyContains: calspermin
Cispecies: Rattus norvegicus (Norway rat)
Cispecies: Rattus norvegicus (Norway rat)
Cispecies: All 103; Ala231; Ala2865; Ala2865, A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Molecule type: DNA
A; Residues: 47-141, NB: 144-474 (OH1>
A; Residues: 47-141, NB: 144-474 (OH1>
A; Cross references: UNIPROT: P13234; GB:M74488; NID:g203219; PIDN:AAA40845.1; PID:g203220
A; Cross reference as been revised in reference A41237
A; Note: part of this sequence was confirmed by sequencing of CDNA to mRNA
B; Ohmstede, C.A.; Bland, M.M.; Merrill, B.M.; Sahyoun, N.
Proc. Natl. Acad. Sci. U.S.A. 88, 9375, 1991
A; Reference number: A41237
A; Reference number: A41237
A; Residues: 142-143 (OH3)
A; Residues: 142-143 (OH3)
A; Residues: 142-143 (OH3)
A; Residues: 142-143 (OH3)
A; Cross references: GB:M6334
A; Cross references: GB:M6334
A; Cross references: GB:M6334
A; Note: this is a revision to the sequence from reference A41103
B; Ohmstede, C.A.; Jensen, K.F.; Sahyoun, N.E.
A; Note: this is a revision to the sequence from reference A41103
A; Note: CAA: Jensen, X.F.; Sahyoun, N.E.
A; Note: Caa. Sci. (24) (Calmodulin-dependent protein kinase enriched in cerebellar granule cells.
A; Reference number: A32865; MUID:89174647; PMID:2538431
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gene 137, 351-352, 1993
A;Title: Identification of alternate 5' untranslated regions in the gene encoding Ca2+/ca
A;Reference number: I53706; MUID:94131312; PMID:8299971
A;Accession: I53706
A;Status: preliminary: translated from GB/EMBL/DDBJ
A;Rolecule type: DNA
A;Rolecule type: DNA
A;Residues: 1-37 <RES>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Cross-references: GB:L16999; NID:g310086; PIDN:AAA17443.1; PID:g310087
C;Comment: Ca2+/calmodulin-dependent protein kinase IV is enriched in cerebellar granule
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Adv. Exp. Med. Biol. 255, 263-268, 1989
A;Title: Calspermin is a testis specific calmodulin-binding protein closely related to
A;Reference number: A60255; MUID:90144189; PMID:2618865
A;Accession: A60255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C;Superfamily: Ca2+/calmodulin-dependent protein kinase; protein kinase homology
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Xseaidues: 306-371, M',373-474 <ON1>
A;Cross-references: GB:J04446; NID:9203642; PIDN:AAA40990.1; PID:9203643
R;Ono, T.; Means, A.R.
277 K-KVEKGKYYFDFNDWKNISEEAKELIKLMLTYDYNKRITAKEALNSKWIK 326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A,Molecule type: protein
A,Residues: 335-363 <0M2>
A,Note: the amino end of calspermin was blocked
R,Bland, M.M.
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g
                                                                                                                                                                                                                                                                                                                                                                                                                                    protein kinase (EC 2.7.1.37) - malaria parasite (Plasmodium falciparum)
N.Alternate names: calcium-dependant protein kinase
C.Species: Plasmodium falciparum
C.Species: Blasmodium falc
C.Species: Rappes, B.; Franklin, R.M.
J. Biol. Chem. 268, 4347-4354, 1993
J. Biol. Chem. 268, 4347-4354, 1993
J. Ritle: Gene structure and expression of an unusual protein kinase from Plasmodium falc
A.Reference number: A45472; MUID:93179444; PMID:8440720
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Molecule type: DNA
A; Residues: 1-524 < CANA
A; Residues: 1-524 < CANA
A; Cross-receas: UNIPROT: Q27731; EMBL: X67288; NID: 99877; PIDN: CAA47704.1; PID: 99878
A; Cross-receas: UNIPROT: Q27731; EMBL: X67288; NID: 99877; PIDN: CAA47704.1; PID: 99878
A; Note: sequence extracted from NCBI backbone (NCBIN: 125849, NCBIP: 125850)
B; Gardner, M.J; Tettellin, H.; Carucci, D.J.; Cummings, L.M.; Aravind, L.; Koonin, E.V.;
Science 282, 1126-1132, 1998
A; Title: Chromosome 2 sequence of the human malaria parasite Plasmodium falciparum.
A; Reference number: A71609; MUID: 99021743; PMID: 9804551
A; Status; nucleic acid sequence not shown; translation not shown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Introns: 406/3; 440/1; 479/3; 505/3
C;Superfamily: calcium-dependent protein kinase; calmodulin repeat homology; protein kin C;Superfamily: calcium-dependent protein king C;Superfamily: calcium-binding: BF hand; phosphotransferase; serine/threonine-specific F;54-325/Domain: protein kinase homology «kin»
F;62-70/Region: protein kinase ATP-binding motif
F;416-448/Domain: calmodulin repeat homology «EF4»
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Molecule type: DNA
*Residues: 1-524 «GAR»
A;Cross-references: GB:AE001419; GB:AE001362; NID:g3845281; PIDN:AAC71952.1; PID:g384528
A;Experimental source: clone 3D7
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                                429 EQAFDLVKNLLVVDPEQRLTTKQALEHPWLQDDSMKHTVERLMYGVDHTMPPPIKKNIIR 488
                                                                            249 GSAKDFITHLMCCDPEARFTCQDALSHPWISGNT----AYTHDIHGTVAVHLKKSLAK 302
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Matches 124; Conservative 6
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Brain Res. Mol. Brain Res. 19, 215-218, 1993
A;Title: Cloning and sequencing of a gene encoding the beta polypeptide of Ca2+/calmodul
A;Reference number: 152637; MUID:94018484; PMID:8412563
A;Accession: 152637
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    calmodulin binding; phosphotransferase; serine/th
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                                                                                                                                                                                                                                                                        15 SSVTSSTENLVPDYWIDGSKRDPLSDFFEVESELGRGATSIVYRCKOKGTOKPYALKVLK 74
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152631
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25pecies: Rattus sp. (rat)
25pecies: Rattus sp. (rat)
25pecies: Aul-1996 #sequence_revision 26-Jul-1996 #text_change 09-Jul-2004
25accession: 152637
R;Sakagami, H; Kondo, H.
                                                                                                                                                                                                                               174 SDLSVDDQTIYPKDFIDK-----YIMSRPIGSGACGEVKLAFQKSVCKKVAVKIIS
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19.7%; Score 534.5; DB 2; Length 5
Best Local Similarity 39.8%; Pred. No. 1.7e-17;
Matches 117; Conservative 52; Mismatches 104; Indels
                                                                                                                                              19.7%; Score 534.5; DB 1; Length ilarity 39.8%; Pred. No. 1.6e-17; Conservative 52; Mismatches 104; Indels
C; Keywords: alternative splicing; ATP; calmodulin bindi P;40-296/Domain: protein kinase homology «KIN» P;48-27/Region: protein kinase ATP-binding motif P;366-474/Product: calspermin #status predicted «CSP» P;318-337/Region: calmodulin binding #status predicted F;71/Active site: Lys #status predicted
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Best Local Similarity
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A;Cross-references: GB:L17000; NID:g306478; PIDN:AAA35639.1; PID:g306479
C;Comment: This protein is a Ca2+-responsive multifunctional protein kinase, which occurs
s system and in the immune system.
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C; Superfamily: Ca2+/calmodulin-dependent protein kinase; protein kinase homology
C; Superfamily: Ca2+/calmodulin-dependent protein kinase homology
C; Keywords: ATP; calcium binding; calmodulin binding; phosphoprotein; phosphotransferase;
F; 44-300/Domain: protein kinase ATP-binding molif
F; 52-60/Region: calmodulin binding #status predicted
F; 8, 12, 15/Binding site: phosphate (Ser) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Accession: JC2261
A;Molecule type: MRNA
A;Residues: 1-473 < KINA
A;Residues: 1-473 < KINA
A;Residues: 1-473 < KINA
A;Cross-references: GB:D30742; NID:g487908; PIDN:BAA06403.1; PID:g871845
Gene 142, 1994
A;Ribland, M.M.; Monroe, R.S.; Ohmstede, C.
Gene 142, 191-197, 1994
A;Title: The cDNA sequence and characterization of the Ca2+/calmodulin-dependent protein
A;Reference number: IS3768; MUID:94252566; PMID:8194751
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CaM kinase-Gr, expressed after tra
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PID:9407006
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     R;Kitani, T.; Okuno, S.; Fujisawa, H.
J. Biochem. 115, 637-640, 1994
A;Title: cDNA cloning and expression of human calmodulin-dependent protein kinase IV.
A;Reference number: JC2261; MUID:94375404; PMID:8089075
                                                                                                                                                                                 A53036

26.24.Callmodulin-dependent protein kinase (BC 2.7.1.123) IV - human
N;Alternate names: Ca2+/calmodulin-dependent protein kinase Gr; CaM-kinase IV
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Accession: A53036; JC2261; I53768
R;Mosialos, G.; Hanissian, S.H.; Jawahar, S.; Vara, L.; Kieff, B.; Chatila, T.A.
A;Title: A Ca(2+)/Calmodulin-dependent protein kinase, CaM kinase-Gr, expressed
A;Reference number: A53036; MUID:94149862; PMID:8107230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 370 TAGTIGYSSAVDCWSLGVILFVCLCGYPPFSEQNSNIPLKNQIAEGKYTYIAAAWRNVSE 429
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               215 GC---AYGPEVDMMSVGIITYILLCGFEPFYDERGDQFMFRRILNCEYYFISPWWDEVSL 271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         44 DPFEVESELGRGAISIVYRCKOKGIOKPYALKVLKKTVDKK-----IVRTBIGVLL 94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GB:L24959; NID:g407005; PIDN:AAA18251.1;
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271 DQFMFRILNCEYYFISPWMDEVSLNAKDLVKKLIVLDPKKRLTTFQALQHPWV 324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 473;
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A,Status: preliminary; translated from GB/EMBL/DDBJ
A,Molecule type: mRNA
A,Residues: 1-473 <RES>
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A,Cross-references: GDB:6155815; OMIM:602366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A,Accession: A53036
A,Status: preliminary
A,Molecule type: mRNA
A,Residues: 1-473 <MSO>
A,Cross-references: UNIPROT:Q16566;
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7;

Gaps

24;

Length 560;

302 136

16

419

193

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420 IAAAWRNVSEQAFDLVKNLLVVDPEQRLTTKQALEHPWLQDDSMKHTVERLMYGVDHTMP 479
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                                                                                                                                                                                                                                                                186 KDFIDKYIMSRPIGSGACGEVKLAFQKSVCKKVAVKIISKRKFKMNTSSNEHPISVDT--
                                                                                                                                                                                                                                                                                                           17 KGFYAKYEPKEILGRGISSTVRRCIEKETGKEFAAKIIDLGATTESGETNPYHMLEATRO
                                                                                                                                                    Query Match 18.7%; Score 506; DB 2; Length 56 Best Local Similarity 35.0%; Pred. No. 3.7e-16; Matches 116; Conservative 57; Mismatches 134; Indels
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                           A; Map position: 10
C; Superfamily: protein kinase homology
C; Reywords: phosphorransferase
F;21-291/Domain: protein kinase homology <KIN>
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A,Cross-references: FlyBase:FBgn0011754
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A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Accession: A53300
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Molecule type: mRNA
A; Molecule type: mRNA
A; Residues: 1-735 < RES>
A; Cross-references: UNIPROT: Q63531; GB: M99169; NID: g206771; PIDN: AA02872.1; PID: g206772
C; Genetics:
A; Genetics:
A; Genetics: ATP; phosphotransferase; serine/threonine-specific protein kinase
C; Keywords: ATP; phosphotransferase; serine/threonine-specific protein kinase
F; 60-221/Domain: protein kinase APP-binding motil
F; 88-76/Region: protein kinase homology < KIN2>
F; 416-675/Domain: protein kinase ATP-binding motil #status atypical
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S51600
Sphosphorylase kinase (EC 2.7.1.38) gamma chain - fruit fly (Drosophila melanogaster)
C;Gecies: Drosophila melanogaster
C;Date: 19-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 16-Aug-2004
C;Accession: S51600
R;Bahri, S.M.; Chia, W
R;Bahri, Genet. 245, 588-597, 1994
A;Title: DPhK-gamma, a putative Drosophila kinase with homology to vertebrate phosphorylutants.
                                                                                                                               C;Species: Rattus norvegicus (Norway rat)
C;Species: So.Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
C;Accession: A53300
R;Grove, J.R.; Price, D.J.; Banerjee, P.; Balasubramanyam, A.; Ahmad, M.F.; Avruch, J.
B;Grove, J.R.; Price, D.J.; Banerjee, P.; Balasubramanyam, A.; Ahmad, M.F.; Avruch, J.
A;Grove, J.R.; Price, D.J.; Banerjee, P.; Balasubramanyam, A.; Ahmad, M.F.; Avruch, J.
A;Title: Regulation of an epitope-tagged recombinant Rsk-1 S6 kinase by phorbol ester an A;Reference number: A53300; MUID:93349850; PMID:7688S67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          440
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                                                                                                         ribosomal protein S6 kinase (EC 2.7.-.-) II - rat
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A;Cross-references: UNIPROT:Q9VYV7; EMBL:U13014; NID:g531470; PIDN:AAA64560.1; PID:g5314 A;Note: the authors translated the codon CAT for residue 528 as Ala and CAC for residue C;Genetics:

A;Gene: FlyBase:PhK-gamma

A; Reference number: S51600; MUID:95107257; PMID:7808409

A, Accession: S51600 A, Molecule type: DNA A, Residues: 1-560 < BAH>

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PRELIMINARY;
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Q918V3;
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1487.331 Million cell updates/sec
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Q7sek0
Q6bh59
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Q9z265
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09hbs5
06qa08
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09hd31
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                                              7, 2005, 12:34:23 ; Search time 178 Seconds
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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                                                                                                                                     1612378 segs, 512079187 residues
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                                                                                                                                                                                                                                                                                                                                           Q98TW0
CHK2 HUMAN
Q9R019
CHK2 MOUSE
Q6QA1
Q9HCQ8
Q9HCQ8
Q90ZY5
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DUN1_YEAST
Q6FKZ8
Q8AVN4
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Q6CPX0
KCC1_MOUSE
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Maximum Match 100%
Listing first 45 summaries
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Guo Z., Dunphy W.G.;

Mol. Biol. Cell 11:1535-1546(2000).

-i - SINILARITY: Belongs to the Ser/Thr protein kinase family.

EMBL; AFI14295; ARF75829.1; --

GO; GO:0005524; F:AFP binding; IEA.

GO; GO:000554; F:protein serine/threonine kinase activity; IEA.

GO; GO:00066740; F:protein amino acid phosphorylation; IEA.
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R InterPro; IPR000253; FHA.
R InterPro; IPR000259; FHA.
R InterPro; IPR000199; Kinase like.
R InterPro; IPR001999; Prot kinase.
R InterPro; IPR008271; Ser_thr_pkinase.
R InterPro; IPR008271; Ser_thr_pkinase.
R InterPro; IPR00894; SMAD_FHA.
R Pfam; PF004089; FHA; I.
R SMART; SM00209; Prinase; 1.
R SMART; SM00220; B TKC; 1.
R PROSITE; PS50006; FHA DOMAIN; 1.
R PROSITE; PS50011; PROTEIN KINASE DOM; 1.
R PROSITE; PS5011] REOTEIN KINASE ST; 1.
R PROSITE; PS5011] REOTEIN KINASE ST; 1.
R PROSITE; PS60109; PROTEIN—KINASE ST; 1.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
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100.0%; Pred. No. 1.4e-164;
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Q8BJX8
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Q6FK01
Q86UH5
Q96WX5
Q97X3
Q77XG
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Q07TSG
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                                                                           1 MMSRDTKTESQQSQGTSSSSSSSAPQSYSQSSSSGTLSSLDTVPVQDLASIPEDPEIDED
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MEDILINE-99055399; PubMed-9836640; DOI=10.1126/science.282.5395.1893;
Matsuoka S., Huang M., Elledge S.J.;
"Linkage of ATW to cell 19vole regulation by the Chk2 protein kinase. Science 282:1893-1897(1998).
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Catarrhini; Hominidae; Homo.
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Brown A.L., Lee C.-H., Schwarz J.K., Mitiku N., Piwnica-Worms H.
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               Length
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            Score 2704; DB 2;
Pred. No. 4.5e-164;
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Mammalia; Eutheria; Primates;
              99.7%;
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Biol. 9:1-10(1999).
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                                                              ELGHGHSRVANIEDLSGNGTFVNKEIIGKGRTLPLTNNAEIALSLPTNKVFVFSDLSVDD
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PEGENT, TROUGS, FHA; U. Pfam; PF00498; FHA; U. Pfam; PF00498; FHA; U. Pfam; PF00069; Pkinase; 1. Probom; PD000001; Prot kinase; 1. SMART; SM00240; FHA; U. SMART; SM00240; FHA; U. PROSITE; PS50006; FHA DOMAIN; 1. PROSITE; PS50011; PROTEIN KINASE DOM; 1. PROSITE; PS00108; PROTEIN KINASE ST; 1. ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase. SEQUENCE 517 AA; :58310 MM; 401A3235AA0BDCBE CRC64;
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
Xenopodinae; Xenopus.
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GO:0004674; F.protein serine/threonine kinase activity; IEA.
GO:0016740; F.transferase activity; IEA.
GO:0006468; P.protein amino acid phosphorylation; IEA.
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SEQUENCE FROM N.A. M., Takisawa H.;
Matsui T., Nakanishi M., Takisawa H.;
Submitted (DEC-2000) to the EMBL/GenBank/DDBJ databases
-I- SIMILARITY: Belongs to the Ser/Thr protein kinase fe
EMBL; AF326577, AGG59884.1; --
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GO; GO: 0004674; F:protein serine/threon.
GO; GO: 0016740; F:protein serine/threon.
GO; GO: 0006468; P:protein amino acid ph.
InterPro; IPR000253; FHA.
InterPro; IPR0011009; Kinase like.
InterPro; IPR001109; Kinase.
InterPro; IPR001109; Ser_thr_pkinase.
InterPro; IPR008291; Ser_thr_pkinase.
InterPro; IPR008984; SMAD_FHA.
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An human Cd3: related kinase that functions downstream of ATM protein for the callular response to DNA damages.";

An human Cd3: related kinase that functions downstream of ATM protein for child. Rel. Acid. Scil. U.S.A. 96.7745.3750(1990).

BEOURNER FROW N. CALL S.A. 96.7745.3750(1990).

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PubMed=11461078; DOI=10.1054/bjoc.2001.1858;
Allinen M., Huusko P., Mantyniemi S., Launonen V., Winqvist R.;
"Mutation analysis of the CHK2 gene in families with hereditary breast -!- DISEASE: Defects in CHEK2 are associated with Li-Fraumeni syndrome (LFS) [MIM:151623]; a highly penetrant familial cancer phenotype usually associated with inherited mutations in p53/TP53.
-!- DISEASE: Defects in CHEK2 are found in some patients with prostate cancer (Cap) [MIM:17682 are found in some patients with osteosarcoma (OSRC) [MIM:259500]. Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
"Generation and initial analysis of more than 15,000 full-length human -!- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
-!- ENZYME REGULATION: Kinase activity is up-regulated by autophosphorylation. Rapidly phosphorylated in response to DNA damage and to replication block.
-!- SUBCELLULAR LOCATION: Nuclear.
-!- TISSUE SPECTIVITY: High expression is found in testis, spleen, colon and peripheral blood leukocytes. Low expression is found in other tissues. MEDLINE=20085462; PubMed=10617473; DOI=10.1126/science.286.5449.2528; Bell D.W., Varley J.M., Szydlo T.E., Kang D.H., Wahrer D.C.R., Shannon K.E., Lubratovich M., Versalis S.J., Isselbacher K.J., Fraumeni J.F., Birch J.W., Li F.P., Garber J.E., Haber D.A.; "Heterozygous germ line hCHK2 mutations in Li-Fraumeni syndrome."; PubMed=11746983; DOI=10.1002/gcc.1207;
Miller C.W., Ikezoe T., Krug U., Hofmann W.K., Tavor S., Vegesna V., Tsukasaki K., Takeuchi S., Koeffler H.P.;
"Mutations of the CHK2 gene are found in some osteosarcomas, but are rare in breast, lung, and ovarian tumors.";
Genes Chromosomes Cancer 33:17-21(2002). Dong X., Wang L., Taniguchi K., Wang X., Cunningham J.M.,
McDonnell S.K., Qian C., Marks A.F., Slager S.L., Peterson B.J.,
Smith D.I., Cheville J.C., Blute M.L., Jacobsen S.J., Schaid D.J.,
Tindall D.J., Thibodeau S.N., Liu W.L., Jacobsen S.J., Schaid D.J.,
Tindallons in CHEKZ associated with prostate cancer risk.",
Am. J. Hum. Genet. 72:270-280(2003)
-!-FUNCTION: Controls cell cycle checkpoint. May participate in
transduction of the DNA damage and replicational stress signals.
Inhibits CDC25C phosphatase by phosphorylating it on Ser-216,
preventing the entry into mitosis. May have a role in meiosis as VARIANTS PROSTATE CANCER LYS-64; PRO-145; ARG-167; CYS-180; HIS-180; CYS-181; HIS-181; LYS-239; PHE-251; HIS-318; PRO-323; CYS-327 AND LYS-476, AND VARIANT THR-157. -!- SIMILARITY: Belongs to the Ser/Thr protein kinase family. CDS1 Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002). VARIANT THR-157, AND VARIANT COLON CANCER TRP-145. VARIANTS OSTEOSARCOMA SER-17 AND LEU-85. -!- SIMILARITY: Contains 1 FHA domain. Br. J. Cancer 85:209-212(2001). Science 286:2528-2531(1999). and mouse cDNA sequences." PubMed=12533788; cancer.

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Q9R019 PRELIMINARY;
Q9R019;
01-MAY-2000 (TrEMBLrel. 13;
01-OCT-2003 (TrEMBLrel. 25;
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entities requires a license agreement (See http://www.isb-sib.ch/announce/
or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61.0%; Score 1655.5; DB 1; Length 543;
59.9%; Pred. No. 2.9e-97;
ive 74; Mismatches 105; Indels 39; Gaps
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                                                    EMBL; AJ131197; CAA10319-1; EMBL; AF066904; AAC83693.1; EMBL; AF066299; AAC83693.1; EMBL; AF066299; AAD11784.1; EMBL; AL117330; CAB62923.1; EMBL; AL117330; CAB62923.1; EMBL; AL121825; CAB62923.1; EMBL; BC04207; AAH04207.1; PDB; IGXC; X-ray; A/D/G/J=64-212. Genew; HGXC:16627; CHEK2. H-InvDB; HIX0016341; -... Reactome; O96017; -... RMIM; 151623; -... MIM; 151623; -... MIM; 259500; -... MIM; 259500; -...
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GO; GO:0006464; F:protein serine/threonine kinase activity; IEA.

GO; GO:0006468; P:protein amino acid phosphorylation; IEA.

GO; GO:0006468; P:protein amino acid phosphorylation; IEA.

IN terPro; IPR01009; Kinase like.

InterPro; IPR000219; FrA.

IN terPro; IPR000219; FrA.

InterPro; IPR000219; Ser_thr_pkinase.

InterPro; IPR000819; Ser_thr_pkinase.

InterPro; IPR00894; SMAD_FHA.

R Pfam; PF00498; FHA; 1.

ProDom; PR000001; Prot_kinase; 1.

R Pfam; PF000001; Prot_kinase; 1.

R SWART; SM00240; FHA; 1.

R PROSITE; PS5001; PROTEIN KINASE DOM; 1.

R PROSITE; PS5001; PROTEIN KINASE ST; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                57 IDEDIPOPWGRLWALGKGFLNHDCLHEEYVFGRDKKCDYTFDIPVLNQTDRYKTYSKRHF
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Rattus.
NCBI_TaxID=10116;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Usage by and for commercial
                                                               KYTYIAAAWRNVSEQAFDLVKNLLVVDPEQRLTTKQALEHPWLQDDSMKHTVERLMYGVD 475
                                                                                                     KYNLIPEVWTDVSEKALDLVKKLLVVDPKARLTTEEALSHPWLQDEHMKKKFQDLLVQEK 506
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=99055399; PubMed=9836640; DOI=10.1126/science.282.5395.1893; Matsuoka S., Huang M., Elledge S.J.; "Linkage of ATM to cell cycle regulation by the Chk2 protein kinase."; Science 282.1893-1897(1998)
and mouse CDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002)
-!- FUNCTION: Controls cell cycle checkpoint. May participate in transduction of the DNA damage and replicational stress signals. Inhibits CDC25 phosphatase by phosphorylating it, preventing the entry into mitcosis. May have a role in maiosis as well.
-!- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoryctein.
-!- BNZYME REGULATION: Kinase activity is up-regulated by autophosphorylation. Rapidly phosphorylated in response to DNA damage and to replication block (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SIMILARITY: Belongs to the Ser/Thr protein kinase family. CDS1
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                     | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | : | | : | : | | : | : | | : | : | | : | : | | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : 
                                                                                                                                                  HTMPPPI--KKNIIRKRGHEWD-QDASTSS----CSEIL 507
                                                                                                                                                                                                                                                                                                                                  30-MAY-2000 (Rel. 39, Created)
COMAY-2000 (Rel. 39, Last sequence update)
05-UTL-2004 (Rel. 44, Last annotation update)
Serine/threonine-protein kinase Chk2 (EC 2.7.1.37)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           use by non-profit institutions as long a modified and this statement is not removed.
                                                                                                                                                                                                                                                                                              546 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                   Name=Chek2; Synonyms=CHK2, Rad53;
                                                                                                                                                                                                                                                                                            STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                      Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=10090;
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                                                                                                                                                                                                                                                                                            CHK2 MOUSE
                                                                                                     447
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                                                                                                                                                                                                                                                                    CHK2_MOUSE
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  (See http://www.isb-sib.ch/announce/
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  246
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      398
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       187
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         367 VLNTAGTTGYSSAVDCWSLGVILFVCLCGYPPFSEQNSNIPLKNQIAEGKYTYIAAAWRN 426
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    427 VSEQAFDLVKNLLVVDPEQRLTTKQALEHPWLQDDSMKHTVERLMYGVDH--TMPPPIKK 484
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          518
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               339 VQYLHENGIIHRDLKPENVLLSSQEEDCLIKITDFGQSKILGETSLMRTLCGTPTYLAPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        399 VLVSNGTAGYSRAVDCWSLGVILFICLSGYPPFSEHKTQVSLKDQITSGKYNFIPEVWTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 40 ELSQYQGSSSSSTGTVPSSSQSSHSSGTLSSLETVSTQELCSIPEDQEPEEPGPAPWAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    128 RVANIEDLSGNGTFVNKEIIGKGRTLPLTNNAEIALSLPTNKVFVFSDLSVDDQTIYPKD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   160 YIVYIEDHSGNGTFVNTELIGKGKRCPLSNNSEIALSLCRNKVFVFFDLTVDDQSVYPKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            188 FIDKYIMSRPIGSGACGEVKLAFQKSVCKKVAVKIISKRKFRMNTSSN-EHPISVDTEIE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            220 LRDEYIMSKTLGSGACGEVKWAFERKTCOKVAIKIISKRRFALGSSREADTAPSVETEIE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ILKKLDHPCIIKIENFFDSEDFYYIVLELMEGGELFDRVVNSTRLREPIAKLYFYQMLLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VQYLHENGVIHRDLKPENVLLSSTSEECCIKITDFGQSKILGETSLMRTLCGTPTYLAPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9 ESQQSQCTSSSSSSSAP-QSYSQSSSSGTLSSLDTVPVQDLASIPEDPEIDEDIPQPWGR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    60.4%; Score 1637; DB 1; Length 546; 63.0%; Pred. No. 4.5e-96;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        similarity)
                                                                                                                                                                                                                                                                                                                                                                         ProDom; PD000001; Prot kinase; 1.
PROSITE; PS50006; FHA DOMAIN; 1.
PROSITE; PS50010; PROTEIN KINASE ATP; FALSE NEG.
PROSITE; PS50011; PROTEIN KINASE DOM; 1.
PROSITE; PS00108; PROTEIN KINASE ST; 1.
ATP-binding; Call cycle; Nuclear protein; Phosphorylation; Serine/threonine-protein kinase; Transferase.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        51 Proton acceptor (By simil: 61088 MW; A7949EFB5572CDAA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Protein kinase.
ATP (By similarity).
ATP (By similarity).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              63.0%; Pred. No. 4.5e
ive 71; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             485 NIIRKRGHEWDQDASTSS-----CSEIL 507
entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                                                                       InterPro; IPR000253; FHA.
InterPro; IPR011009; Kinase_like.
InterPro; IPR000109; Proct kinase.
InterPro; IPR008271; Ser_thr_pkin_AS.
InterPro; IPR008984; SMAD_FHA.
Pfam; PF00498; FHA; 1.
Pfam; PF00069; Pkinase; 1.
                                                                            EMBL; AF086905; AAC83694.1;
EMBL; BC056617; AAH56617.1;
HSSP; O96017; IGXC.
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                                                                                                                                                              MGD; MGI:1355321; Chek2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         253 2
351 3
546 AA;
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tes 320; Conserv
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                                       ETSLMRTLCGTPTYLAPEVLNTAGTTGYSSAVDCWSLGVILFVCLCGYPPFSEQNSNIPL 408
      230 MNTSSNEHP-ISVDTEIEILKKLDHPCIIKIENFFDSEDFYYIVLELMEGGELFDRVVNS 288
                                                                                                                                                                                                                                                                                                                                                              409 KNQIAEGKYTYIAAAWRNVSEQAFDLVKNLLVVDPEQRLTTKQALEHPWLQDDSMKHTVE 468
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       360 KRLKEATCKLYFYQMLLAVQYLHENGIIHRDLKPENVLLSSQEEDCLIKITDFGHSKILG
                                                                                                                                                                                                                                                                            420 ETSLMRTLCGTPTYLAPEVLVSVGTAGYNRAVDCWSLGVILFICLSGYPPFSEHRTQVSL
                                                                                                                                                                                                                                                                                                                                                                                               289 TRLREPIAKLYFYOMLLAVOYLHENGVIHRDLKPENVLLSSTSEECCIKITDFGQSKILG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Craniata; Vertebrata; Euteleostomi;
Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q9HCQ8;
01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-MAR-2001 (TrEMBLrel. 27, Last annotation update)
CHK2 (Protein Kinase Chk2 transcript variant del9) (Fragment)
Name=Chk2; Synonyms=CHK2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          55.1%; Score 1499; DB 2; Length 514; 55.5%; Pred. No. 2.6e-87; ive 72; Mismatches 102; Indels 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            469 RLMYGVDHTMPPP---IKKNIIRKRGHEWDQDASTSS-----CSEIL 507
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GO; GO:0005524; F:ATP binding; IEA.
GO; GO:0004672; F:protein kinase activity; IEA.
GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
Ogawa A., Okabe-Nakamura A.;
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           514 514
514 AA; 57525 MW; 8B99B81830B8092F CRC64;
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PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
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Pfam; PF00069; Pkinase; 1.
ProDom; PD00001; Prot_kinase; 1.
SMART; SM00240; FHA; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR000253; FHA.
InterPro; IPR011009; Kinase like.
InterPro; IPR000719; Prot kinase.
InterPro; IPR008984; SMAD_FHA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity 55.5
Matches 302; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (Human)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SSLDTVPVQDLASI----PEDPEIDEDIPQPWGRLWALGKGFLNHD------
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                                                                                                                                                                                                                                                                                                                                                        Staalesen V., Falck J., Geisler S., Bartkova J., Borresen-Dale A.-L.,
Lukas J., Lillehaug J.R., Lonning P.E.;
Submitted (FEB-2004) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Е.Л.,
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SWART; SM00240; FHA; 1.
SWART; SM00219; TYKG; 1.
SWART; SM00219; TYKG; 1.
PROSITE; PS50006; FHA DOMAIN; 1.
PROSITE; PS50011; PROTEIN KINASE DOM; 1.
PROSITE; PS00108; PROTEIN KINASE ST; 1.
ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
skoilence 586 AA; 65418 MW; 55BDE42C9A0F98A7 CRC64;
                                                                                                                                                                    Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Colling J.E., Wright C.L., Edwards C.A., Davis M.P., Grinham J.A, Cole C.G., Goward M.E., Aguado B., Mallya M., Mokrab Y., Huckle E Beare D.M., Dunham I.;
Submitted (MAY-2004) to the EMBL/GenBank/DDBJ databases.
-- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
EMBL; MS51297; AAS584581; --
EMBL; CR456418; CAG30304.1; --
HSSP; Q63450; 1A06.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GO; GO:0005524; F:ATP binding; IEA.
GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.
GO; GO:0016740; F:transferase activity; IEA.
GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   82;
05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
Proctein kinase Chk2 transcript variant insX (CHEK2 protein).
Name=CHK2; Synonyms=CHEK2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 586;
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55.5%; Pred. No. 3.3e-95;
.ive 74; Mismatches 105; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR000253; FHA.
InterPro; IPR000253; FHA.
InterPro; IPR000719; Prot kinase.
InterPro; IPR000719; Prot kinase.
InterPro; IPR008219; Ser_thr_pkinase.
InterPro; IPR008271; Ser_thr_pkinase.
InterPro; IPR00894; SMAD_FHA.
InterPro; IPR001245; Tyr_pkinase.
Ffam; PF00498; FHA; 1.
Pfam; PF00498; FHA; 1.
ProDom; PD000001; Prot_kinase; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity 55.5
Matches 326; Conservative
                                                                                                                                                                                                                                                                                                                            TISSUE=Breast carcinoma;
                                                                                                                                                        Homo sapiens (Human).
                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
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STRAIN=B; TISSUE=Whole body;

X STRAIN=B; TISSUE=Whole body;

A Straubberg R.L., Pergod B.A., Grouse L.H., Derged J.G.,

Klausherg R.L., Peingold E.A., Grouse L.H., Derged J.G.,

A Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.R., Schuler G.D.,

A Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.R., Bhat N.K.,

A Diatchenko L., Marusina K.P., Farmer A.A., Wabin G.M., Hong L.,

B Diatchenco M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

B Rownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

R Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

B Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

R Pahey J., Helton B., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

M Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

B Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   QELGHGHSRVANIEDLSGNGTFVNKEIIGKGRTLPLTNNAEIALSLPTNKVFVFSDLSVD 179
                                                                                                                                                                                                                                                                                                                                                                                                   YFYQMLLAVQYLHENGVIHRDLKPENVLLSSTSEECCIKITDFGQSKILGETSLMRTLCG 358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TPTYLAPEVLNTAGTTGYSSAVDCWSLGVILFVCLCGYPPFSEQNSNIPLKNQIAEGKYT 418
                                                                                                                                                                                                                                                                                                                                                     66 VQPQVWGRIIPLKQGFSVLNCTENQYSFGRDKRCDYSFSNSILKKSPYFNTYSKKHFRIF
                                                                                                                                                                                                                      DQTIYPKDFIDKYIMSRPIGSGACGEVKLAFQKSVCKKVAVKIISKRKF-KMNTSSNEHP
                                                                                                                                                                                                                                                                                    DOANLPLEFSKKYHIARKIGTGVCGEVKLAIEKETFKKVALKTINKHDFPSIGTATR---
                                                                                                                                                                                                                                                                                                                                    239 ISVDTEIEILKKLDHPCIIKIENPFDSEDFYYIVLELMEGGELFDRVVNSTRLREPIAKL
                                                                                                                                                                                                                                                                                                                                                                                                                     DIPQPWGRLWALGKGFLNHDCLHEEYVFGRDKKCDYTFDIPVLNQTDRYKTYSKRHFRIF
                                                                    3 SRDTKTESQ-QSQGTSSSSSSAPQSYSQ--SSSSGTLSSLDTVPVQDLASIPEDPEIDE
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Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
Cyprinidae; Danio.

NCBI_TaxID=7955;
     503;
     Length
   48.6%; Score 1317.5; DB 2; Length 53.7%; Pred. No. 9.1e-76; ive 86; Mismatches 125; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-JUN-2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
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475 NOPMRPEATRKR 486
                                   Conservative
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                      Similarity
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                                  264;
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   Query Match
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Q803E2;
                       Local
                      Best Loca
Matches
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                                                                                                                                                240
                                                                                                                                                                                 271
                                                                                                                                                                                                    241 KTCKKVAIKIISKRKFAIGSAREADPALNVETEIELLKKLNHPCIIKIKNFFDAED-YYI 299
                                                                                                                                                                                                                                                  331
                                                                                                                                                                                                                                                                   300 VLELMEGGELPDKVVGNKRLKEATCKLYFYQMLLAVQ------336
                                                                                                                                                                                                                                                                                                                 EECCIKITDFGQSKILGETSLMRTLCGTPTYLAPEVLNTAGTTGYSSAVDCWSLGVILFV 391
                                                                                                                                                                                                                                                                                                                                     ----ITDFGHSKILGETSLMRTLCGTPTYLAPEVLVSVGTAGYNRAVDCWSLGVILFI 390
                                                                                                                                                                                                                                                                                                                                                                                  CLCGYPPFSEQNSNIPLKNQIAEGKYTYIAAAWRNVSEQAFDLVKNLLVVDPEQRLTTKQ 451
                                                                                                                                                                                                                                                                                                                                                                                                    503
CDYTFDIPVLNOTDRYKTYSKRHFRIFQELGHGHSRVANIEDLSGNGTFVNKEIIGKGRT
                                                                    181 RPLNNNSEIALSLSRNKVFVFFDLTVDDQSVYPKALRDEYIMSKTLGSGACGEVKLAFER
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Actinopterygii, Neopterygii, Teleostei, Ostariophysi, Cypriniformes,
Cyprinidae, Danio.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
SEQUENCE 503 AA; 56699 MW; BC01BF3D8E4CEC71 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ZFIN; ZDB-GENE-030131-8942; zgc:55865.
GO; GO:0005524; F:ATP binding; IEA.
GO; GO:000464; F:protein serine/threonine kinase activity; IEA.
GO; GO:0016740; F:transferase activity; IEA.
GO; GO:001668; P:protein amino acid phosphorylation; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Chou C.-M., Leu J.-H., Huang C.-J.;
Submitted (MAY-2000) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
EMBL; AF265346; AAK52419.1; -.
AFSP; P49137; INX.
ZFIN; ZDB-GENE-030131-8942; zgc:55865.
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Last annotation update)
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Pfam, PF00069; Pkinase; 1.
Probom, PD000001; Prot_kinase; 1.
SMART; SM00240; FHA, 1.
SMART; SM00220; S_TKC; 1.
PROSITE; PS50066; FHA_DOMAIN; 1.
PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
PROSITE; PS0011; PROTEIN_KINASE_ST; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
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PRELIMINARY;
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                                                                                                                                                                                                        NCBI_TaxID=9606;
                                                                                                                                                           Name=CHK2;
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                                                     RESULT 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                66 VQPQVWGRTIPLKQGFSVLNCTENQYSFGRDKRCDYSFSNSILKKSPYFNTYSKKHFRIF 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     179
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 59
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Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S., Krzywinski M.I., Skalabka U., Smailus D.E., Schnerch A., Schein J.E., Jones S.J., Marra M.A.; "Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          38 -NAEREIEILKKIDHPCLIKTEDFYQTEDSYYIVLEYIEGGELFGRIKAKKLEEDIAKL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            297 YFYQMLKAVEYLHNNGIIHRDLKPENVLLASHDDICLIKITDFNQSKILEESSLMKTLCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TPTYVAPEVFTHASTVGYTKAVDYWSLGVLLFICLGGYPPFNTECTTMSVREQIINGEYR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               QELGHGHSRVANIEDLSGNGTFVNKEIIGKGRTLPLTNNAEIALSLPTNKVFVFSDLSVD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DQTIYPKDFIDKYIMSRPIGSGACGEVKLAFQKSVCKKVAVKIISKRKF-KMNTSSNEHP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         239 ISVDTEIEILKKLDHPCIIKIENFFDSEDFYYIVLELMEGGELFDRVVNSTRLREPIAKL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               YFYQMLLAVQYLHENGVIHRDLKPENVLLSSTSEECCIKITDFGQSKILGETSLMRTLCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3 SRDTKTESQ-QSQGTSSSSSSAPQSYSQ--SSSSGTLSSLDTVPVQDLASIPEDPEIDE
                                                                                                                                                                                                                                                                                                                                                                  SMART; SM00240; FHA, 1.
SMART; SM00220; S TKC; 1.
PROSITE; PS50006; FHA DOMIN; 1.
PROSITE; PS50011; PROTEIN KINASE DOM; 1.
PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
ATP-binding; Kinase; Serine, threshouse, Coccin kinase; Transferase.
                                                                                    SERAIN-AB; TISSUE=Whole body;
STRAIN-AB; TISSUE=Whole body;
STRAIN-AB; TISSUE=Whole body;
Straubsberg R.;
Submitted (JAN-2003) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
EMBL; BC044519; AAH44519.1; -.
ZENS; P49137; INXK.
ZENS; P49137; INXK.
ZENS; PA9137; INXK.
ZENS; PA9137; INXK.
GO; GO:0005524; F:ATP binding; IEA.
GO; GO:0006740; F:Transferase activity; IEA.
GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 2; Length 503;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           48.4%; Score 1311.5; DB 2; Length 53.7%; Pred. No. 2.2e-75; rive 84; Mismatches 127; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                  503 AA; 56657 MW; 351A24EA5BBAF8D5 CRC64;
                                                                 Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
                                                                                                                                                                                                                                             InterPro; IPR000253; FHA.
InterPro; IPR000253; FHA.
InterPro; IPR001009; Kinase like.
InterPro; IPR000719; Proc Kinase.
InterPro; IPR0002290; Ser thr pkinase.
InterPro; IPR008271; Ser thr pkinase.
InterPro; IPR008271; Ser thr pkin AS.
IREAPRO; IPR008984; SMAD FHA.
Pfam; PF00499; FHA.
                                                                                                                                                                                                                                                                                                                                                       ProDom; PD000001; Prot_kinase; 1.
                                                 and mouse cDNA sequences."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity 53.7%
Matches 264; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PPPIKKNIIRKR 490
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               213 SVCKKVAVKIISKRKFKGANTSSNEHP-ISVDTELEILKKLDHPCIIKIENFFDSEDFYYI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 MSRDTKTESQ-------QSQGTSSSSSSSAP-QSYSQSSSGTL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 MSRESDVEAQQSHGSSACSQPHGSVTQSQGSSSQSQGISSSSTSTMPNSSQSSHSSSGTL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             153 LPLTNNAEIALSLPTNKVFVFSDLSVDDQTIYPKDFIDKYIMSRPIGSGACGEVKLAFQK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VLELMEGGELFDRVVNSTRLREPIAKLYFYQMLLAVQYLHENGVIHRDLKPENVLLSSTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TISSUE-Breast carcinoma, Staalesen V., Falck J., Geisler S., Bartkova J., Borresen-Dale A.-L., Lukas J., Lillehaug J.R., Lonning P.E.; Submitted (FEB-2004) to the EMBL/GenBank/DDBJ databases.
-! SIMILARITY: Belongs to the Ser/Thr protein kinase family.
EMBL, AY551303; AAS58464.1; --.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PEDMI PF00069; PKINASH, I.
Proban; PR00001; Prot kinase; 1.
SMART; SM00209; TKK; 1.
SMART; SM00219; TyrKc; 1.
SMART; PS00101; PROTEIN KINASE DOM; 1.
ATP-binding; Kinase; Serinc'threonine-protein kinase; Transferase.
SEQUENCE 452 AA; 50202 MW; 96F70353E4F3C85B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hashing Go. 0004674; F. Protein serine/threonine kinase activity; IEA. GO; GO.0004674; F. Protein serine/threonine kinase activity; IEA. GO; GO.0004713; F. Protein-tyrosine kinase activity; IEA. GO; GO.00046740; F. Protein amino acid phosphorylation; IEA. InterPro; IPR011009; Kinase like.

InterPro; IPR00129; For Linase.

InterPro; IPR002290; Ser thr pkinase.

InterPro; IPR002271; Ser_thr_pkinase.

InterPro; IPR002271; Ser_thr_pkinase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
47.5%; Score 1287; DB 2; Length 452;
Best Local Similarity 49.6%; Pred. No. 7e-74;
Matches 270; Conservative 56; Mismatches 88; Indels 130;
                                                                                                                                                                                                                                             05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Protein kinase Chk2 transcript variant del2-3.
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475 NOPMRPEATRKR 486
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240 DLVKKLLVVDPKARFTTEEALRHPWLQDEDMKRKFQDLLSEENESTALPQVLAQPSTSRK 299
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CDYTFDIPVLNQTDRYKTYSKRHFRIFQELGHGHSRVANIEDLSGNGTFVNKEIIGKGRT 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      153 LPLTNNAEIALSLPTNKVFVFSDLSVDDQTIYPKDFIDKYIMSRPIGSGACGEVKLAFQK 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     38 SSLDTVPVQDLASI----PEDPEIDEDIPQPWGRLWALGKGFLNHDCLHEEYVFGRDKK 92
                       DLVKNLLVVDPEQRLTTKQALEHPWLQDDSMKHTVERLMYGVDHTMPPP---IKKNIIRK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  213 SVCKKVAVKIISKRKFKMNTSSNEHP-ISVDTEIEILKKLDHPCIIKIENFFDSEDFYYI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bartkova J., Borresen-Dale A.-L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2 MSRDTKTESQ-------GSGGTSSSSSSAP-QSYSQSSSGTL
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A Staalesen V., Falck J., Geisler S., Bartkova J., Borresen-Dale A.-L.

A Lukas J., Lilehaug J.R., Lonning P.B.;

Lukas J., Lilehaug J.R., Lonning P.B.;

Submitted (FEB-2004) to the EMBL/GenBank/DDBJ databases.

EMBL; AY551300; AA558461.1;

R GO; GO:00004674; FrATP binding; IEA.

R GO; GO:00004674; FrATP binding; IEA.

R GO; GO:0000468; P:Protein serine/threonine kinase activity; IEA.

R GO; GO:0000468; P:Protein amino acid phosphorylation; IEA.

R InterPro; IPR00109; Kinase like.

R InterPro; IPR0019; Prote kinase.

R InterPro; IPR002290; Ser thr_pkinase.

R InterPro; IPR00984; SMAD_FHA.

R Pfam; PF00498; FHA; 1.
                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
VCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     37.3%; Score 1012.5; DB 2; Length 339; 60.2%; Pred. No. 1.5e-56; ive 47; Mismatches 56; Indels 31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                339 AA; 38125 MW; CAE0E58DF0308393 CRC64;
                                                                                                                                                                                                                                                                                             05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Protein kinase Chk2 transcript variant del9-12.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     272 VLELMEGGELFDRVVNSTRLREPIAKLYFYQMLLAVQ 308
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                                                                                                                                                                                                                                                        339
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SMART; SM00240; FHA; 1.
PROSITE; PS50006; FHA DOMAIN; 1.
PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
                                                                                                                                300 RPREGEAEGAETTKRPAVCAAVL 322
                                                                                                        490 RGHEWDQDASTSS----CSEIL 507
                                                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches 203; Conservative
                                                                                                                                                                                                                                                        PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                            Q6QA08;
05-JUL-2004 (
05-JUL-2004 (
                                                                                                                                                                                                                                                                                                                                                                                  Name=CHK2;
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                       433
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                                                                                                                       CLSGYPPFSEHRTOVSLKDQITSGKYNFIPEVWAEVSEKALDLVKKLLVVDPKARFTTEE 388
                                                                                                                                                                                           61 HPCIIKIKNFFDAED-YYIVLELMEGGELFDKVVGNKRLKEATCKLYFYQMLAVQYLHE 119
                     451
                                                                                                                                                                 ALEHPWLQDDSMKHTVERLMYGVDHTMPPP---IKKNIIRKRGHEWDQDASTSS----C 503
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  194 MSRPIGSGACGEVKLAFQKSVCKKVAVKIISKRKFKMNTSSNEHP-ISVDTEIEILKKLD 252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     312
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  373 TTGYSSAVDCWSLGVILFVCLCGYPPFSEQNSNIPLKNQIAEGKYTYIAAAWRNVSEQAF 432
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EECCIKITDFGQSKILGETSLMRTLCGTPTYLAPEVLNTAGTTGYSSAVDCWSLGVILFV
                                                                                CLCGYPPFSEQNSNIPLKNOIAEGKYTYIAAAWRNVSEQAFDLVKNLLVVDPEQRLTTKQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   253 HPCIIKIENFFDSEDFYYIVLELMEGGELFDRVVNSTRLREPIAKLYFYQMLLAVQYLHE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         R HISSP, P4913/; INAX.

GO; GO:0005524; F:ArDer binding; IEA.

GO; GO:0004674; F:prore binding; IEA.

R GO; GO:00046740; F:prore bin serine/threonine kinase activity; IEA.

R GO; GO:0016740; F:transferase activity; IEA.

R GO; GO:00166468; P:protein amino acid phosphorylation; IEA.

R GO; GO:0006468; P:protein amino acid phosphorylation; IEA.

R GO; GO:0006468; P:protein amino acid phosphorylation; IEA.

R GO; GO:0006468; P:protein Ainase.

R InterPro; IPR000219; Prot Kinase.

R InterPro; IPR00021; Ser thr pkinase.

R ProDom; P0000001; Prot Kinase; 1.

R MART; SM00220; S TKC; 1.

R PROSITE; PS00108; PROTEIN KINASE DOM; 1.

R PROSITE; PS00108; PROTEIN KINASE ST; 1.

W ATP-binding; Hypothetical protein; Kinase;

Serine/threonine-protein kinase; Transferase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gu J.R., Wan D.F., Zhao X.T., Zhou X.M., Jiang H.Q., Zhang P.P., Qin W.X., Huang Y., Qiu X.K., Qian L.F., He L.P., Li H.N., Yu Y., Yu J., Han L.H., Han L.H., Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases.

-- SIMLARITY: Belongs to the Ser/Thr protein kinase family.

EMBL, AP217975; AAG17218.1; --

HSSP; P49137; INXK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 322;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           63; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                           Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 39.3%; Score 1066; DB 2;
Best Local Similarity 63.8%; Pred. No. 5.4e-60;
Matches 206; Conservative 44; Mismatches 63
                                                                                                                                                                                                                                                                                                                                                                                                      322 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                         01-MAR-2001 (TrEMBLrel. 16, 01-MAR-2001 (TrEMBLrel. 16, 01-OCT-2003 (TrEMBLrel. 25,
                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hypothetical protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                              : : |
449 AAVL 452
                                                                                                                                                                                                                                                    504 SEIL 507
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=9606;
                                                                                                                          329
                                       269
                                                                                                                                                                 452
                                                                                                                                                                                                          389
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                                                                                392
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                                                                                                                                                                                                                                                                                                                                                                                                    09HBS5
                                                                                                                                                                                                                                                                                                                                                    RESULT 11
Q9HBS5
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DO VIELMEGGELFERVVORMELAERATCHIPTCHALANG 316

RESULT 13

LOW BROONE STANDARD; EPRT; 476 AA.

LOW DROWN STANDARD; EPRT; 476 AA.

COURT STANDARD; CARREST STANDARD; EPRT; 476 AA.

DO STANDARD STANDARD; EPRT; 476 AA.

TO STANDARD STANDARD; EPRT; 476 AA.

DO STANDARD STANDARD; EPRT; 476 AA.

TO STANDARD STANDARD; EPRT; 476 AA.

DE STANDARD STANDARD; EPRT; 476 AA.

DE STANDARD STANDARD STANDARD; EPRT; 476 AA.

NOTE TAXADARD STANDARD STAN
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GO; GO:0005634; C:nucleus; IEP.
GO; GO:0004674; F:protein serine/threonine kinase activity; NAS.
GO; GO:0000077; P:DNA damage response, signal transduction re. . .; IMP.
GO; GO:0008630; P:DNA damage response, signal transduction re. . .; IMP.
GO; GO:0007281; P:germ-cell development; IEP.
GO; GO:0006468; P:protein amino acid phosphorylation; NAS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TISOURCE OF TABLE TO SEQUENCE = VSP 004865; both isoforms are TISSUE SPECIFICITY: In stage 3 embryos, both isoforms are expressed in both somatic and pole cell nuclei. Expression in pole cell nuclei is sustained until stage 9 and weakly expressed after pole cell invagination into the abdominal cavity. DEVELOPMENTAL STAGE: Expressed both maternally and zygotically in adult females. Levels of the long isoform remain fairly constant from ovaries to embryos, the levels of short isoform decrease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN=Berkeley; TISSUE=Embryo; MEDINTE-22426066; PubMed=12537569; Medinter R.A., Guarin H., Kronmiller B., Pacleb J.M., Park S., Wan K.H., Rubin G.M., Celniker S.E.; Genome Biol. 3:RESEARCH0080.1-RESEARCH0080.1-RESEARCH0080.1-RESEARCH0080.1-RESEARCH0080.1-RESEARCH0080.1-RESEARCH0080.1-RESEARCH0080.1-RESEARCH0080.1-RESEARCH0080.1-RESEARCH0080.1-RESEARCH0080.1-RESEARCH0080.1-RESEARCH0080.1-RESEARCH0080.1-RESEARCH0080.1-RESEARCH0080.1-RESEARCH0080.1-RESEARCH0080.1-RESEARCH0080.1-RESEARCH0080.1-RESEARCH0080.1-RESEARCH0080.1-RESEARCH0080.1-RESEARCH0080.1-RESEARCH0080.1-RESEARCH0080.1-RESEARCH0080.1-RESEARCH0080.1-RESEARCH0080.1-RESEARCH0080.1-RESEARCH0080.1-RESEARCH0080.1-RESEARCH0080.1-RESEARCH0080.1-RESEARCH0080.1-RESEARCH0080.1-RESEARCH0080.1-RESEARCH0080.1-RESEARCH0080.1-RESEARCH0080.1-RESEARCH0080.1-RESEARCH0080.1-RESEARCH0080.1-RESEARCH0080.1-RESEARCH0080.1-RESEARCH0080.1-RESEARCH0080.1-RESEARCH0080.1-RESEARCH0080.1-RESEARCH0080.1-RESEARCH0080.1-RESEARCH0080.1-RESEARCH0080.1-RESEARCH0080.1-RESEARCH0080.1-RESEARCH0080.1-RESEARCH0080.1-RESEARCH0080.1-RESEARCH0080.1-RESEARCH0080.1-RESEARCH0080.1-RESEARCH0080.1-RESEARCH0080.1-RESEARCH0080.1-RESEARCH0080.1-RESEARCH0080.1-RESEARCH0080.1-RESEARCH0080.1-RESEARCH0080.1-RESEARCH0080.1-RESEARCH0080.1-RESEARCH0080.1-RESEARCH0080.1-RESEARCH0080.1-RESEARCH0080.1-RESEARCH0080.1-RESEARCH0080.1-RESEARCH0080.1-RESEARCH0080.1-RESEARCH0080.1-RESEARCH0080.1-RESEARCH0080.1-RESEARCH0080.1-RESEARCH0080.1-RESEARCH0080.1-RESEARCH0080.1-RESEARCH0080.1-RESEARCH0080.1-RESEARCH0080.1-RESEARCH0080.1-RESEARCH0080.1-RESEARCH0080.1-RESEARCH0080.1-RESEARCH0080.1-RESEARCH0080.1-RESEARCH0080.1-RESEARCH0080.1-RESEARCH0080.1-RESEARCH0080.1-RESEARCH0080.1-RESEARCH0080.1-RESEARCH0080.1-RESEARCH0080.1-RESEARCH0080.1-RESEARCH0080.1-RESEARCH0080.1-RESEARCH0080.1-RESEARCH0080.1-RESEARCH0080.1-RESE
                                                                                                                       GENOME REANNOTATION, AND ALTERNATIVE SPLICING.
MEDLINE=22426069; PubMed=12537572;
Mista S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochnik S.E.,
Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Berman B.P.,
Bettencourt B.R., Celniker S.E., de Grey A.D. N.J., Drysdale R.A.,
Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,
Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         dramatically. SHOOMS to the Ser/Thr protein kinase family. CDS1
                                                                                                                                                                                                                                                                                                                                                                                                            "Annotation of the Drosophila melanogaster euchromatic genome: a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Genome Biol. 3:RESEARCH0083.1-RESEARCH0083.22(2002).
Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C., "The genome sequence of Drosophila melanogaster."; Science 287:2185-2195(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Event=Alternative splicing; Named isoforms=2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IsoId=O61267-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     subfamily.
-!- SIMILARITY: Contains 1 FHA domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR000719; Prot kInase.
InterPro; IPR008271; Ser Thr pkin AS.
InterPro; IPR002290; Ser thr pkinase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A. (ISOFORM SHORT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR010053; FHA.
InterPro; IPR011009; Kinase_like.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL, AB007821, BAA28755.1; -. EMBL, AB007822, BAA28756.1; -. EMBL, U87984; AAB49642.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HSSP, Q16539; 1КV1.
FlyBаве; FBgn0019686; lok.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       systematic review.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Name=Short;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Name=Long;
                                                                                                                                                                                                                                                                                                                                                                                            Lewis S.E.
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EMBL; ;
HSSP; (
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61 SSLETVSTQELYSIPEDQEPEDQEPEEPTPAPWARLWALQDGFANLECVNDNYWFGRDKS 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CDYTFDIPVLNQTDRYKTYSKRHFRIFQELGHGHSRVANIEDLSGNGTFVNKEIIGKGRT 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SSLDTVPVQDLASI-----PEDPEIDEDIPQPWGRLWALGKGFLNHDCLHEEYVFGRDKK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           153 LPLTNNAEIALSLPTNKVFVFSDLSVDDQTIYPKDFIDKYIMSRPIGSGACGEVKLAFQK
                                                                                            Bartkova J., Borresen-Dale A.-L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TLDSSSSSSSAP-QSYSQSSSSSSSSSSCTL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     30; Gaps
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Galagan J.B., Calvo S.E., Borkovich K.A., Selker E.U., Read N.D.,
Jaffe D., FitzHugh W., Ma L.-J., Smirnov S., Purcell S., Rehman B.,
Jaffe D., FitzHugh R., Wang S., Nielsen C.B., Butler J., Endrizzi M.,
Qui D., Ianakiev P., Pedersen D., Nelson M., Washburne M.,
Selitrennikoff C.P., Kinsey J.A., Braun E.L., Zelter A., Schulte U.,
Kothe G.O., Jedd G., Mewes W., Staben C., Marcotte E., Greenberg D.,
Roy A., Foley K., Naylor J., Thomann N., Barrett R., Gnerre S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Neurospora crassa.
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Sordariomycetidae; Sordariales; Sordariaceae; Neurospora.
                                                                                                                                                       Length 289;
     Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                29.2%; Score 791; DB 2; Length 28: 56.4%; Pred. No. 1.6e-42; ive 42; Mismatches 51; Indels
                                                     SEQUENCE FROM N.A.
TISSUE=Breast carcinoma;
Staalesen V., Falck J., Geisler S., Bartkova J., Borress
Lukas J., Lillehaug J.R., Lonning P.E.;
Submitted (FEB-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; AYS51298; AASS8459.1;
                                                                                                                                                                                                                                                                                                                                                                                                               289 AA; 32141 MW; 630D0AF3AE5114E6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               241 KTCKKVAIKIISKRKFAIGSAREADPALNVETEIEILKKINH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           213 SVCKKVAVKIISKRKFKMNTSSNEHP-ISVDTEIELLKKLDH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Last sequence update)
Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-MAR-2004 (TrEMBLrel. 201-MAR-2004 (TrEMBLrel. 201-MAR-2004 (TrEMBLrel. 201-MAR-2004 (TrEMBLrel. 201-MYDCUhetical protein. Name=NCU02014.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity 56.4
Matches 159; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                               Kinase.
SEQUENCE
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Q7SEK0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   218 VAVKIISKRKFK-MNTSSN-EHPISVDTEIEILKKLDHPCIIKIENFFDSEDFYYIVLEL 275
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEGGELFDRVVNSTRLREPIAKLYFYQMLLAVQYLHENGVIHRDLKPENVLLSSTSEECC 335
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           336 IKITDFGQSKILGETSLMRTLCGTPTYLAPEVLNTAGTTGYSSAVDCWSLGVILFVCLCG 395
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     396 YPPFSEQNSNIPLKNQIAEGKYTYIAAAWRNVSEQAFDLVKNLLVVDPEQRLTTKQALEH 455
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        438
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                158 NAEIALSLPTNKVFVFSDLSVDDQTIYPKDFIDKYIMSRPIGSGACGEVKLAFQKSVCKK 217
                                                                                                                                                                                                                                                                                                                                                                                                                                                  61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      200 FAMKIVKKOMISGARPSTNFSDPDRVINEAKIMKNLSHPCVVRMHDIVDKPDSVYMVLEF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   320 LKVSDFGLSKFVQKDSVMRTLCGTPLYVAPEVLITGGREAYTKKVDIWSLGVVLFTCLSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       62 PQPWGRLWALGKGF-------DINFOLHEEYVFGRDKKCDYTF---DI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100 P--VLNQTDRYKTYSKRHFRIFQELGHGHSRVANIEDLSGNGTFVNKEIIGKGRTLPLTN
                                                                                                                                                                                                                                                                                                                                                                                                                                                MSRDTKTESQQSQCTSSSSSSAPQSYSQSSSGGTLSSLDTVPVQDLASIPEDPEIDEDI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                               74;
                                                                                                                                                                                                                                                                                    Proton acceptor (By similarity) Missing (in isoform Short).
                                                                                                                                                                                                                                                                                                                                                                          30.5%; Score 828; DB 1; Length 476; 36.8%; Pred. No. 1.3e-44;
                                                                                                                                                                                                                                                                                                                                                                                                             90; Mismatches 162; Indels
                                                                                                                                                                                                                                                                                                                       /FTId=VSP_004865.
58D583E015C4E626 CRC64;
                                              Probom; From Processing Strain, From Probom; Probom; Probom; SMART; SM00240; FHA; 1.
SMART; SM00240; FHA; 1.
FROSTIE: PSS0006; FHA DOMIN; 1.
PROSITE; PSS00107; PROTEIN KINASE ATP; 1.
PROSITE; PS00109; PROTEIN KINASE DOM; 1.
PROSITE; PS00109; PROTEIN KINASE DOM; 1.
Alternative splicing; ATP-binding; Nuclear protein; Serine/threonine-protein kinase; Transferase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q6QA10 PRELIMINARY, PRT; 289 AA. Q6QA10; COALU-2004 (TrEMBLrel. 27, Created) O5-JUL-2004 (TrEMBLrel. 27, Last sequence update) O5-JUL-2004 (TrEMBLrel. 27, Last annotation update) Protein kinase Chk2 transcript variant del7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         456 PWLQDDSMKHTVERLM----YGVDHTMPPPIKKN 485
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 439 SWLRDAPMLQKAKRLMKLDGMEIEEENFLEPPTKRS 474
                                                                                                                                                                                                                                                 ATP (By similarity)
ATP (By similarity)
                                                                                                                                                                                                                                  Protein kinase
                                                                                                                                                                                                                                                                                                                                         54261 MW;
InterPro; IPR008984; SMAD_FHA.
Pfam; PF00498; FHA; 1.
Pfam; PF00069; Pkinase; 1.
                                                                                                                                                                                                                                                                                                                                                                                                             Matches 190; Conservative
                                                                                                                                                                                                                                                                                                    62
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                                                                                                                                                                                                                                                                                                                                         476 AA;
                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity
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                                                                                                                                                                                                                             DOMAIN
NP BIND
BINDING
ACT SITE
VARSPLIC
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                                                                                                                                                                                                                DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           143
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GSGACGEVKLAFQKSVCKKVAVKIISKRKFKANTSSNEHPISVDTEIEILKKLDHPCIIK 258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       259 IENFEDSEDFYYIVLELMEGGELFDRVVNSTRLREPIAKLYFYQMLLAVQYLHENGVIHR 318
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AVDCWSLGVILFVCLCGYPPFSEQ -- NSNIP -- LKNQIAEGKYTYIAAAWRNVSEQAFDL 434
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AVDVWSLGVVLYICLCGFPPFSDELTSPDFPYSLSDQIRQGKFDYPSPYWDPVDDLALDL 531
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          435 VKNLLVVDPEQRLTTKQALEHPWLQ-----DDSMKHTVERLMYGVDHTMPPPIKKNIIR 488
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       68
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GTSSSSSSAPQSYSQSSSGTLSSLDTVPVQDLASIPE----DPEIDEDIPQ-PWGRL
Krystofova S., Rasmussen C., Metzenberg R.L., Perkins D.D., Kroken S., Cogoni C., Macino G., Catcheside D., Li W., Pratt R.J., Osmani S.A., DeSouza C.C., Glass L., Orbach M.J., Berglund J., Voelker R.J., Osmani S.A., Yarden O., Plamann M., Seiler S., Dunlap J., Radford A., Aramayo R., Natvig D.O., Alex L.A., Mannhaupt G., Ebbole D.J., Freitag M., Paulsen I., Sachs M.S., Lander B.S., Nusbaum C., Birren B.; Mature O.O. (2003).

"The Genome Sequence of the Filamentous Fungus Neurospora crassa."; Nature O.O. (2003).

-!- SIMILARITY: Belongs to the Ser/Thr protein kinase family.

-!- SIMILARITY: Bequence shown here is derived from an high speliminary data.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ::
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                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL, AABXOLO0031;
HSSP; PAP9137; LNXK.
HSSP; PAP9137; LNXK.
GO; GO:0005524; F:AFP binding; IEA.
GO; GO:0005547; F:Protein serine/threonine kinase activity; IEA.
GO; GO:000648; P:protein serine/threonine kinase activity; IEA.
GO; GO:000648; P:protein serine/threonine kinase activity; IEA.
InterPro; IPR000253; FHA.
InterPro; IPR00109; Kinase like.
InterPro; IPR00109; Kinase like.
InterPro; IPR008291; Ser thr pkin_AS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels 101;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ------KGFLNHDCLHEE-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    26.8%; Score 727.5; DB 2; Length 712; 32.8%; Pred. No. 5.4e-38; tive 95; Mismatches 168; Indels 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ..
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PROSTIE; PSS0006; FHA DOWAIN; 1.
PROSTIE; PSS00107; PROTEIN KINASE DOM; 1.
PROSTIE; PSS0011; PROTEIN KINASE DOM; 1.
PROSTIE; PS00108; PROTEIN KINASE ST; 1.
ATP-binding; Hypothetical protein; Kinase;
Serine/threonine-protein kinase; Transferase.
SEQUENCE 712 AA; 79186 WW; ASEA2536542B339B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR008984; SMA<mark>D</mark>
Pfam; PF00498; FHA; 1.
Pfam; PF00069; Pkinase; 1.
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Best Local Similarity
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Db 532 IDSMLVVDPEKRFTIDDCLSHPWMTQKTPGVNDSTNGLVNGIA-GLDVT-----RRGVLR 585
Qy 489 KR 490
:|
Db 586 ER 587
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Search completed: July 7, 2005, 13:02:14 Job time : 182 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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OM protein - protein search, using sw model

July Run on:

7, 2005, 12:33:18; Search time 162 Seconds (without alignments) 1234.291 Million cell updates/sec

US-10-618-173-2 Title:

Perfect score:

1 MMSRDTKTESQQSQGTSSSS.....ASTSSCSELLPTSAEKRAKR 517 Seguence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

2105692 seqs, 386760381 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

geneseqp2002s:* geneseqp2003as:* geneseqp2003bs:* geneseqp2004s:* A Geneseq 16Dec04:* geneseqp1980s:* geneseqp1990s:* geneseqp2000s:* geneseqp2001s:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		40				
Result No.	Score	Query	Query Match Length	DB	ID	Description
	2712	100.0	517	Ŋ	AAB47789	Aab47789 Protein k
8	1656	61.1	542	4	AAG68375	Aag68375 Human Chk
e.	1655.5	61.0	543	~	AAY06204	Aay06204 Human che
4	1655.5	61.0	543	~	AAY05765	Novel
ß	1655.5	61.0	543	ഗ	AAM48995	_
9	1655.5	61.0	543	Ŋ	ABG30701	Human
7	1655.5	61.0	543	ω	ADL32561	
6 0	1655.5	61.0	543	œ	ADM72213	Adm72213 Human TAS
σ	1655.5	61.0	543	œ	ADO44010	Ado44010 Amino aci
10	1655.5	61.0	543	ω	ADQ09232	
11	1651.5	60.9	543	ហ	AAM48996	Aam48996 Human Chk
12	1643.5	9.09	543	ო	AAY67968	Aay67968 Human cel
13	1624	59.9	586	ω	ADN61455	Adn61455 Human KPP
. 14	1499	55.3	514	S	AAM48994	Aam48994 Human Chk
15	1499	55.3	514	80	ADL32563	Adl32563 Human Chk
16	838.5	30.9	459	4	ABB65298	Abb65298 Drosophil
17	621	22.9	513	80	ADN18925	Adn18925 Bacterial
18	603	22.2	356	4	AAB84360	Aab84360 Amino aci
19	600.5	22.1	355	4	AAB50055	Aab50055 Murine De
	600.5	22.1	355	4	AAE11777	Aae11777 Human kin
21	600.5	22.1	355	4	AAM41268	Aam41268 Human pol
22	600.5	22.1	355	ស	ABB08178	Abb08178 Human CaM
23	600.5	22.1	357	4	AAE11768	Aae11768 Human kin
24	600.5	22.1	357	80	ADJ75440	Adj75440 Marker ge
25	600.5	22.1	357	œ	ADQ15044	Adq15044 Human can

Aam39482 Human pol Aab84359 Amino aci Aau03508 Human pro Adc15044 Calcium/c Abg65794 Human CAM Aas34492 Human CAM Adp23704 Human CAM Adp23704 Human CAM Adp23704 Human CAM Abg65792 Human CAD Aae22764 Human CAD Aae22764 Human CAD Aae22764 Human CAD Aae56391 Human Pro Add56398 Human Pro Add45328 Human Pro Add45328 Human Pro Add45328 Human Bro Add45328 Human Bro Add4525 Human ser Add4525 Human ser Add4526 Rat Protee	
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ALIGNMENTS

AAB47789 standard; protein; 517 AA RESULT 1 AAB47789

AAB47789; X A X B X B X

(first entry) 04-MAR-2002

Protein kinase Cds1.

Protein kinase; Xenopus; Cds1; Xcds1; DNA damage checkpoint; cell cycle; Cdc25; forkhead-associated domain; FHA domain; ATM; ATR; DNX-PK; Chk2; human; mitotic delay.

Xenopus laevis.

WO200183703-A2.

08-NOV-2001.

04-MAY-2001; 2001WO-US014646.

04-MAY-2000; 2000US-0202028P

(CALY) CALIFORNIA INST OF TECHNOLOGY.

Dunphy WG, Guo Z;

WPI; 2002-066528/09. N-PSDB; AAI72072.

Novel polypeptide for regulating cell cycle progression, which is activated and phosphorylated in response to double-stranded DNA useful for diagnosing and treating cell proliferative disorder.

Claim 2; Fig 2; 75pp; English.

This sequence shows the protein kinase, Xenopus Cdal (Xcdal) which plays a role in DNA damage checkpoint and regulating progression of cell cycle. The protein is characterized as phosphorylating Cdc25 or its homolog, having a molecular mass of \$\$E\text{KD}\$. \$57 amino acids, \$\$Q\$/TQ motifs at the amino terminal region, a carboxyl terminal kinase domain and an amino Ser287 in the 14-3-3 binding site, which inhibits its activity. Xcdal is activated by poly(dT)40. When Xcdsl is phosphorylated in extracts containing poly(dT)40. When Xcdsl is phosphorylated in extracts increase over background in its kinase activity towards GST-Cdc25[254-316]-WT. The \$\$Q\$/TQ motifs at the amino terminal end of Xcdsl are

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potential substrates for kinases such as ATM, ATR and DNX-PK that are involved in checkpoint pathways. The C-terminal kinase domain is the most conserved region of Xcds1 when compared to ChK2, the human homologue of Xcds1. Cds1 protein or mRNA is useful for diagnosing a Cds1-associated disorder in a subject, by determining the level of Cds1 in the subject expression in the subject, where a low level of Cds1 in the subject compared to a control is indicative of a Cds1-associated disorder. Oligonucleotides (see AAI72073-75) which form double stranded regions with Xcds DNA are useful for increasing mitotic delay in a vertebrate cell.
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cell proliferation; apoptosis.
                                                                                                                                                                                                                                                                                                                                              61 IPQPWGRLWALGKGFLNHDCLHEEYVFGRDKKCDYTFDIPVLNQTDRYKTYSKRHFRIFQ
                                                                                                                                                                                                                                                                                                                                                                                                        ELGHGHSRVANIEDLSGNGTFVNKEIIGKGRTLPLTNNAEIALSLPTNKVFVFSDLSVDD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      QTIYPKDFIDKYIMSRPIGSGACGEVKLAFQKSVCKKVAVKIISKRKFKMYSSNEHPIS
                                                                                                                                                                                                                                                                                              MMSRDTKTESQQSQGTSSSSSSAPQSYSQSSSSGTLSSLDTVPVQDLASIPEDPEIDED
                                                                                                                                                                                                                                                                                                                                                                                        ELGHGHSRVANIEDLSGNGTFVNKEIIGKGRTLPLTNNAEIALSLPTNKVFVFSDLSVDD
                                                                                                                                                                                                                                                                                                                                                                                                                                                    QTIYPKDFIDKYIMSRPIGSGACGEVKLAFQKSVCKKVAVKIISKRKFKMNTSSNEHPIS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            YQMLLAVQYLHENGVIHRDLKPENVLLSSTSEECCIKITDFGQSKILGETSLMRTLCGTP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYLAPEVLNTAGTTGYSSAVDCWSLGVILFVCLCGYPPFSEQNSNIPLKNQIAEGKYTYI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYLAPEVLNTAGTTGYSSAVDCWSLGVILFVCLCGYPPFSEQNSNIPLKNQIAEGKYTYI
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                                                                                                                                                                                                                                                                                                                             I PQPWGRLWALGKGFLNHDCLHEEYVFGRDKKCDYTFDI PVLNQTDRYKTYSKRHFRI FQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAAWRNVSEQAFDLVKULLVVDPEQRLTTKQALEHPWLQDDSMKHTVERLMYGVDHTMPP
                                                                                                                                                                                                                                     Gaps
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                                                                                                                                                                                                       Length 517;
                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              517
                                                                                                                                                                                                     Query Match 100.0%; Score 2712; DB 5; Best Local Similarity 100.0%; Pred. No. 8e-248; Matches 517; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PIKKNIIRKRGHEWDQDASTSSCSEILPTSAEKRAKR
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                                                                                                                                                                        Sequence 517 AA;
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                                                                                                                                                                                                             The present invention describes a number of peptides which disrupt the G2 cell cycle checkpoint when administered to a cell. They act by inhibiting Chk2 (the sequence of which is shown here) and Chk1 kinases, and may be derived from Cdc25C. The peptides are useful in the treatment of cell proliferation diseases, such as cancer, as the inhibition of the Chks allows DNA damage and induces apoptosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ---SSSSSSAP-QSYSQSSSSGTLS
                                                                                                                                                                                                                                                                                                                                                                                              DYTFOIPVLNQTORYKTYSKRHFRIFQELGHGHSRVANIEDLSGNGTFVNKEIIGKGRTL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    214 VCKKVAVKIISKRKFKMNTSSNEHP-ISVDTEIEILKKLDHPCIIKIENFFDSEDFYYIV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 241 TCKKVAIKIISKRKFAIGSAREADPALNVETEIEILKKLNHPCIIKIKNFFDAED-YYIV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LELMEGGELFDRVVNSTRLREP1AKLYFYQMLLAVQYLHENGV1HRDLKPENVLLSSTSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ECCIKITDFGQSKILGETSLMRTLCGTPTYLAPEVLNTAGTTGYSSAVDCWSLGVILFVC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LSGYPPFSEHRTQVSLKDQITSGKYNFIPBVWAEVSEKALDLVKKLLVVDPKARFTTEEA
                                                                                                                                                   or
                                                                                                                                                                                                                                                                                                                                                                                                                                 SLDTVPVQDLASI----PEDPEIDEDIPQPWGRLWALGKGFLNHDCLHEEYVFGRDKKC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PLTNNAEIALSLPTNKVFVFSDLSVDDQTIYPKDFIDKYIMSRPIGSGACGEVKLAFQKS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LCGYPPFSEQNSNIPLKNQIAEGKYTYIAAAWRNVSEQAFDLVKNLLVVDPEQRLTTKQA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LEHPWLQDDSWKHTVERLMYGVDHTMPPP---IKKNIIRKRGHEWDQDASTSS----CS
                                                                                                                                     Isolated or recombinant polypeptide of 7-11 amino acids, useful for treating cell proliferative disorders, e.g. to stop the growth of, or kill cancer cells, by disrupting the G2 cell cycle arrest checkpoint.
                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                     38;
                                                                                                                                                                                                                                                                                                                             61.1%; Score 1656; DB 4; Length 5 60.0%; Pred. No. 1.4e-147; ive 74; Mismatches 105; Indels
                                                                                                                                                                                        Disclosure; Page 26; 126pp; English
21-SEP-2000; 2000WO-IB001438
                       99JP-00269398.
                                                                                                                                                                                                                                                                                                                                                                               MSRDTKTESQQSQGTS-
                                                                                                                                                                                                                                                                                                                                         Best Local Similarity 60.0
Matches 326; Conservative
                                                                                     Kawabe T;
                                                                                                              WPI; 2001-343125/36.
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                                                                                                                                                                                                                                                                                                     Sequence 542 AA;
                                                             (CANB-) CANBAS
                       22-SEP-1999;
30-NOV-1999;
                                                                                     Suganuma M,
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RESULT 3

WO200121771-A2

29-MAR-2001

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98WO-EP006982.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Luyten WHML, Parker AE;
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540 AAVL 543
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                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                             hCDS1, that acts in coordination with Cdc25 in the DNA damage checkpoint. The sequence is predicted from a CDNA (see AAX88793) isolated from a SK-N-MC neuroblastoma cDNA library. The predicted protein is 28% identical to the cdc1 protein of S. pombe. A 2.2 kb transcript is expressed in testis and in 8 human cancer samples examined. hCDS1, its inhibitors and activators, are useful for treating cancer or proliferative disease (claimed). Inhibitors and activators of the kinase activity can also be used in anti-cancer therapy, particularly by increasing susceptibility of cancer cells to chemotherapy and/or radiotherapy (claimed). hCDS1 is useful for modifying DNA damage checkpoint activity of a cancer cell
                                                                                                                                                                                                                                                                                                                                    New human kinase used for treatment of cancer and proliferative diseases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CDYTFDIPVLNOTDRYKTYSKRHFRIFQELGHGHSRVANIEDLSGNGTFVNKEIIGKGRT 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LPLTNNAEIALSLPTNKVFVFSDLSVDDQTIYPKDFIDKYIMSRPIGSGACGEVKLAFQK 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            181 RPLNNNSEIALSLSRNKVFVFFDLTVDDQSVYPKALRDEYIMSKTLGSGACGEVKLAFER 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          241 KTCKKVAIKIISKRKPAIGSARBADPALNVETEIELLKKLNHPCIIKIKNFFDAED-YYI 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         272 VLELMEGGELFDRVVNSTRLREPIAKLYFYQMLLAVQYLHENGVIHRDLKPENVLLSSTS 331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 MSRDTKTESQ------QSQGTSSSSSSSAP-QSYSQSSSGTL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            213 SVCKKVAVKIISKRKFKMNTSSNEHP-ISVDTBIBILKKKLDHPCIIKIENFFDSEDFYYI
                                                                                         Checkpoint kinase; hCDS1; human; DNA damage; proliferative disease;
                                                                                                                                                                                                                                                                                                                                                                                    The present sequence represents a novel human checkpoint kinase,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 2; Length 543;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61.0%; Score 1655.5; DB 2; Length
59.9%; Pred. No. 1.6e-147;
ive 74; Mismatches 105; Indels
                                                                                                                                                                                                                                                                             Luyten WHML, Parker AE, Mcgowan C, Blasina A;
  ¥.
 AAY06204 standard; protein; 543
                                                                                                                                                                                                                                                                                                                                                            Claim 9; Fig 2; 39pp; English.
                                                                    Human checkpoint kinase hCDS1
                                                                                                                                                                                               98WO-EP006981
                                                                                                                                                                                                                     97GB-00022320
                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity 59.9
Matches 326; Conservative
                                                                                                                                                                                                                                           (SCRI ) SCRIPPS RES INST.
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                                                                                                                                                                                                                                                                                                                N-PSDB; AAX58793
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 543 AA;
                                                                                                        cancer; therapy
                                                                                                                                                   WO9925843-A2.
                                              16-AUG-1999
                                                                                                                                                                                               21-OCT-1998;
                                                                                                                                                                                                                     22-OCT-1997;
                                                                                                                            Homo sapiens
                                                                                                                                                                         27-MAY-1999.
                       AAY06204;
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The present sequence represents hCDS1, a novel human cell cycle checkpoint kinase that acts in coordination with Cdc25 at the DNA damage checkpoint, rather than the replication checkpoint as found in yeast. The hCDS1 sequence was predicted from hCDS1 sDNA (see AAZS464) that was checkpoint, with cds1 protein of S. pombe, 28% identity to RAD53 and 27% identity with cds1 protein of S. pombe, 28% identity to RAD53 and 27% clentity to the DWA kinase of S. cerevisiae. Northern blot analysis clentity to the DWA kinase of S. cerevisiae. Northern blot analysis clentified a single transcript of about 2.2 kb expressed in testis and in 8 human cancer samples examined. The characterisation of horsi and the clencidation of its role in the DNA damage checkpoint allows for the proparation of pharmacuticals and therapeutic methods for acting as an adjunct to chemotherapy of cancer. Thus, pharmaceutical formulations incorporating hCDS1 cDNA, RNA, antisense molecules, hCDS1 protein, assays of the invention, can be administered in conjunction with any suitable chemotherapy agent to act as an adjunct to the main action of the chemotherapy agent
                                                                                                                                                                                                                                                                                                                                                                                                                   479
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       539
300 VLELMEGGELFDKVVGNKRLKEATCKLYFYQMLLAVQYLHENGIIHRDLKPENVLLSSQE 359
                                                                                                                                                                                                                                                                                                                             451
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            human cell cycle checkpoint kinase hCDS1, useful for treating cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            332 EECCIKITDFGQSKILGETSLMRTLCGTPTYLAPEVLNTAGTTGYSSAVDCWSLGVILFV
                                                                                                                                                                                                                                                                                                                         392 CLCGYPPFSEQNSNIPLKNQIAEGKYTYIAAAWRNVSEQAFDLVKNLLVVDPEQRLTTKQ
                                                                                                                                                                                                                                                                                                                                                                             420 CLSGYPPFSEHRIQVSLKDQITSGKYNFIPEVWABVSEKALDLVKKLLVVDPKARFTTEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ALEHPWLQDDSWKHTVERLMYGVDHTMPPP---IKKNIIRKRGHEWDQDASTSS----C
                                                                                                                                                                                                  360 EDCLIKITDFGHSKILGETSLMRTLCGTPTYLAPEVLVSVGTAGYNRAVDCWSLGVILFI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            proliferation diseases, e.g. cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Novel human checkpoint kinase hCDS1.
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ALEHPWIQDDSMKHTVERLMYGVDHTMPPP---IKKNIIRKRGHEWDQDASTSS----C 503
                                                                                                                                                                                                                                                          SSLDTVPVQDLASI----PEDPEIDEDIPQPWGRLWALGKGFLNHDCLHEEYVFGRDKK 92
                                                                                                                                                                                                                                                                                                                                                                                                      CDYTPDIPVLNQTDRYKTYSKRHFRIFQELGHGHSRVANIEDLSGNGTFVNKEIIGKGRT
                                                                                                                                                                                                                                                                                                                                                          153 LPLTNNAEIALSLPTNKVFVFSDLSVDDQTIYPKDFIDKYIMSRPIGSGACGEVKLAFQK
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                                                                      The present invention provides the protein and coding sequences of a human Chkz phosphoenzyme inhibitor. The sequences can be used in the chemotherapy of cancers. The present sequence is a protein described the exemplification of the invention
                                                                                                                                                                                     Gaps
       New gene encoding a protein for inhibiting human Chk2 phosphoenzyme activity.
                                                                                                                                                                                  39;
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                                                                                                                                                             Length
                                                                                                                                                          61.0%; Score 1655.5; DB 5; Length
59.9%; Pred. No. 1.6e-147;
.ive 74; Mismatches 105; Indels
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                                                Disclosure; Page 20-23; 36pp; Japanese
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Best Local Similarity 59.9
Matches 326; Conservative
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MSRESDVEAQQSHGSSACSQPHGSVTQSQGSSSQSQGISSSSTSTWPNSSQSSHSSSGTL
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                                                                        -----QSQGTSSSSSSAP-QSYSQSSSGTL
                                                 Gaps
                                                39;
                          Length 543;
                        61.0%; Score 1655.5; DB 2; Length
59.9%; Pred. No. 1.6e-147;
ive 74; Mismatches 105; Indels
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N-PSDB; AAL44750.
                        Query Match
Best Local Similarity
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AAVL 543
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Sequence 543 AA,
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                                               Matches 326;
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419

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The invention relates to an antisense compound targeted to a nucleic acid molecule encoding human checkpoint Kinase 2 (CHK2). The antisense compound specifically hybridises with and inhibits the expression of human CHK2. The antisense compounds are useful as research reagents and diagnostics, in distinguishing between functions of various members of a blological pathway, and in the treatment of a disease or disorder, which can be treated by modulating the expression of CHK2. This sequence
                                                                                                                                                                                                                                                 New antisense oligonucleotides targeted to a nucleic acid encoding checkpoint kinase 2 (CHK2), useful for treating a disease or condition associated with CHK2, or in distinguishing functions of members of a biological pathway.
                                                                                                                                                                                                                                                                                                                                             Disclosure, Page 87-90; 100pp; English
                                                  17-DEC-2001; 2001WO-US048966
                                                                                  22-DEC-2000; 2000US-00746043
                                                                                                                  (ISIS-) ISIS PHARM INC
                                                                                                                                                                        Cowsert LM;
                                                                                                                                                                                                        WPI; 2002-575367/61.
                                                                                                                                    (ABBO ) ABBOTT LAB
                                                                                                                                                                                                                        N-PSDB; ABK88909
                04-JUL-2002
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39; 61.0%; Score 1655.5; DB 5; Length 543; 59.9%; Pred. No. 1.6e-147; 74; Mismatches 105; Indels Matches 326; Conservative Local Similarity Sequence 543 AA; Query Match

539 120 180 LPLTNNAEIALSLPTNKVFVFSDLSVDDQTIYPKDFIDKYIMSRPIGSGACGEVKLAFQK 212 240 271 299 331 391 360 EDCLIKITDFGHSKILGETSLMRTLCGTPTYLAPEVLVSVGTAGYNRAVDCWSLGVILFI 419 451 479 503 CDYTFDIPVLNQTDRYKTYSKRHFRIFQELGHGHSRVANIEDLSGNGTFVNKEIIGKGRT 152 300 VLELMEGGELFDKVVGNKRLKEATCKLYFYOMLLAVOYLHENGIIHRDLKPENVLLSSQE 359 37 9 92 SSLDTVPVQDLASI ----PEDPEIDEDIPQPWGRLWALGKGFLNHDCLHEEYVFGRDKK VLELMEGGELFDRVVNSTRLREPIAKLYFYQMLLAVQYLHENGVIHRDLKPENVLLSSTS -----QSQGTSSSSSSAP-QSYSQSSSGTL MSRESDVEAQQSHGSSACSQPHGSVTQSQGSSSQSQGISSSSTSTMPNSSQSSHSSSGTL SVCKKVAVKIISKRKFKMNTSSNEHP-ISVDTEIELLKKLDHPCIIKIENFFDSEDFYYI EECCIKITDFGQSKILGETSLMRTLCGTPTYLAPEVLNTAGTTGYSSAVDCWSLGVILFV CLCGYPPFSEQNSNIPLKNOIAEGKYTYIAAAWRNVSEQAFDLVKNLLVVDPEQRLTTKQ ALEHPWLODDSMKHTVERLMYGVDHTMPPP---IKKNI IRKRGHEWDODASTSS----C Gaps MSRDTKTESQ----N 38 153 181 213 241 272 332 392 420 480 93 452 엄 ద g g 엄 ò g g ⋧ ò a 셤 δ à ð ð ò à

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detection; cancer; 8q22.3; chromosome 8; human; EDD; tumour suppressor; cell cycle modulator; DNA repair; DNA damage; nuclear targeting protein; progesterone receptor; cytostatic; gene therapy; squamous cell carcinoma; hepatocellular carcinoma; ovarian cancer; breast cancer; melanoma; head and neck cancer; adenocarcinoma; squamous lung cancer; gastrointestinal cancer; renal cell cancer; bladder cancer; prostate cancer; non-squamous carcinoma; glioblastoma; medullablastoma;
                                                                                                            Human Chk2 transcript variant 1 protein SEQ ID NO:19.
                                                          ADL32561 standard; protein; 543 AA
                                                                                                                                                                                                                                                           05-SEP-2003; 2003WO-AU001164
                                                                                                                                                                                       Chk2 transcript variant 1.
                                                                                          (first entry
504 SEIL 507
                540 AAVL 543
                                                                                                                                                                                                                         WO2004022750-A1
                                                                                                                                                                                                         Homo sapiens.
                                                                                          03-JUN-2004
                                                                           ADL32561;
                                         RESULT 7
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Detecting a cancer cell in a subject sample, also related to cancer treatments, comprises determining the level of nucleic acid that is linked to map position 8422.3 of the human genome or its expression

Clancy J, Henshall S;

Henderson M,

Sutherland R, O'brien Saunders D,

Watts C,

WPI; 2004-248472/23.

N-PSDB; ADL32560

(GARV-) GARVAN INST MEDICAL RES. 05-SEP-2002; 2002AU-00951346. 07-NOV-2002; 2002US-0425218P.

Claim 29; SEQ ID NO 19; 331pp; English.

The present invention describes a method for detecting a cancer cell in a subject, which comprises determining the level of nucleic acid that is linked to map position 8q22.3 of the human genome or its expression product in a sample of the subject, where an elevated level of the nucleic acid or polypeptide is indicative of cancer in the subject. Also described: (1) a method for diagnosing a cancer or predicting recurrence of a cancer in a subject comprising determining the level of mRNA or protein encoded by a nucleic acid as described above; (2) the isolated nucleic acid molecule for detecting cancer cell; (3) an isolated or recompliant protein complex, (4) an antibody that binds to the protein complex, complex; (5) a kit for detecting or producing a protein complex, complishing an EDD polypeptide or a portion of an EDD polypeptide and a second polypeptide selected from a protein having cull cycle modulatory activity, a protein associated with DNA repair or damage, a nuclear targeting protein, and a progesterone receptor protein or its portion, where the portion of the protein of an EDD polypeptide; (6) methods for isolating the protein complex; (7) a method for determining a predisposition for disease, or disease state; (8) a method for determining a medialence of the activity, a protein complex; (7) a method for determining a medialence of the activity, a method for determining a medialence of the activity, and a method for determining a medialence of the activity, and a method for determining a medialence of the activity, and a method for determining a medialence of the activity, and a method for determining a medialence of the activity, and a method for determining a medialence of the activity, and a method for determining a medialence of the activity, and a medialence of the activity o formation or stability of an isolated or recombinant protein complex; (9) a method for determining a modulator of the level of protein complex formation; (10) a method for treating a condition associated with

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acid, ribozyme, peptide nucleic acid (PNA), interfering RNA or siRNA, and ribozyme, peptide nucleic acid (PNA), interfering RNA or siRNA, and ribozyme, PNA, interfering RNA or siRNA. EDD has cytostatic activity, and can be used in gene therapy. The methods and modulator are useful for treating a condition associated with EDD over expression such as cancer, e.g. squamous cell carcinoma, hepatocellular carcinoma, ovarian cancer, breast cancer, melanoma, head and neck cancer, adenocarcinoma, squamous lung cancer, gastrointestinal cancer (e.g. gastric, colon, or pancreatic cancer), renal cell cancer, bladder cancer, prostate cancer, non-squamous cancer), renal cell cancer, bladder cancer, prostate cancer, non-squamous composition are useful for reducing the expression of EDD in a cell to inhibit cellular proliferation. The present sequence represents human chk2 transcript variant 1 protein, which is used in the exemplification of the present invention.
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MSRESDVEAQQSHGSSACSQPHGSVTQSQGSSSQSQGISSSSTSTMPNSSQSSHSSSGTL
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 expression of EDD protein in a cell; (11) an antisense
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The invention relates to new isolated tumour-associated kinase (TASK) antolaic acid molecules and encoded polypeptides. Cytostatic. The antibody, oligopeptide or organic molecule that binds to the TASK polypeptide are useful for treating a mammal having a tumour comprising cells expressing the polypeptide. Antagonists of TASK are useful for treating or preventing a cell proliferative disorder (e.g. cancer) associated with increased expression or activity of TASK polypeptide. The TASK polymucleotides and polypeptides may be used as hybridization probes for isolating full length TASK DNA, for generating transgenic animals, in represents a human TASK polypeptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             121 CEYCFDEPLLKRIDKYRTYSKKHFRIFREVGPKNSYIAYIEDHSCNGTFVNTELVGKGKR 180
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                                                                                                                                                                                                                                                                                                                                                               New tumor-associated kinase nucleic acids and polypeptides, useful as hybridization probes for isolating full length TASK DNA, for generating transgenic animals, in chromosome identification, or for tissue typing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            181 RPLNNNSEIALSLSRNKVFVFFDLTVDDQSVYPKALRDEYIMSKTLGSGACGEVKLAFER
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 543;
TASK; tumour-associated kinase; cytostatic; tumour antigen; cell proliferative disorder; cancer; transgenic; human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61.0%; Score 1655.5; DB 8; Length
59.9%; Pred. No. 1.6e-147;
ive 74; Mismatches 105; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 12; SEQ ID NO 18; 163pp; English
                                                                                                                                                                                                                                                                         8
                                                                                                                                                                                                                                                                         Zhang
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                                                                                                                                                                                                   11-SEP-2002; 2002US-0410166P.
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Matches 326; Conservative
                                                                                                                                                                                                                                                                         Desauvage FJ, Wood WI,
                                                                                                                                                                                                                                     (GETH ) GENENTECH INC
                                                                                                                                                                                                                                                                                                           2004-282985/26.
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                                                        sapiens
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37 9 92 271

299

391 419 451

ADM72213 standard; protein; 543 AA.

RESULT 8

17-JUN-2004 (first entry) Human TASK108 polypeptide

ADM72213

ADM72213
ID ADM7
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AC ADM7
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AC ADM7
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DT 17-J
XX
DE Hume

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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The specification describes protein complexes involved in cellular processes which have been shown to be critical for the development of various forms of neurological diseases. Three protein complexes were identified: ASK2 protein complex, Pellino-1 protein complex and Pellino-3 protein complex. The protein complex are useful for treating diseases and plasorders, e.g. stroke, neurodegeneration such as Wallerian degeneration, Alzheimer's disease, neurological disorders such as epilepsy, and inflammatory conditions such as ulcerative colitis, Crohn's disease or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New complex comprising at least one first protein, and at least one second protein, useful for treating stroke, Alzheimer's disease, neurological disorders such as epilepsy, and inflammatory conditions such
                                                                            503
Nek9; PAR3; Pellino 1; Pellino 3; podocalyxin-like protein 1 precursor; Pushover; S-adenosylhomocysteinase; secretory carrier-associated membrane protein 2; surfeit locus protein 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         protein complex; neurological disease; stroke; neurodegeneration; Wallerian degeneration; Alzheimer's disease; neurological disorder; epilepsy; inflammatory condition; ulcerative colitis; Crohn's disease; atherosclerosis; ID-MYO-inositol triphosphate 3 kinase A; ASK1; ASK2; ASK3; CaMKII beta; CaMKII delta; CaMKII gamma; casein kinase II alpha; Cdc37; CHK2; CTCL tumour antigen SE20-4; EF-1 alpha 1; EMAP; FLJ14653 NT2RP2002252; FLJ30839 FEBRA202429; HERC2; inositol polyphosphate-5-phosphatase; inositol-1; 4; Striphosphate; Striphosphate; IRAK1; IRAK1; IRAK4; KIAA1441; MSTP030;
                                                                       ALEHPWLQDDSMKHTVERLMYGVDHTMPPP---IKKNIIRKRGHEWDQDASTSS----C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Schirle M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ubiquitin carboxyl terminal hydrolase 11;
upstream regulatory element binding protein 1; Vartul;
Werner's syndrome helicase interacting protein; WHIP;
X-ray repair cross complementing protein 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Jackson D, Helftenbein G,
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                                                                                                                                                                                                                                                                                                                                             Ä
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Amino acid sequence of human CHK2.
                                                                                                                                                                                                                                                                                                                                     ADO44010 standard; protein; 543
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12-SEP-2002; 2002EP-00020496.
12-SEP-2002; 2002EP-00020497.
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                                                                                                                                                                                                                                                                                                                                                                                                                                   15-JUL-2004 (first entry)
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Kuester B, Hopf C;
                                                                                                                                                                     SEIL 507
                                                                                                                                                                                                                 AAVL 543
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ID ADO4

AAC ADO4

XX ADO4

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atherosclerosis. Proteins identified as being part of the protein complexes of the invention are 1D-MYO-inositol triphosphate 3 kinase A, ASK1, ASK2, ASK3, CaMKII beta, CaMKII delta, CaMKII gamma, casein kinase II alpha, Cdc37, CHK2, CTCL tumour antigen SE20-4, EF-1 alpha 1, EMAP, FLJ14653 NT2RP2002252, FLJ30839 FEBRA2002429, HERC2, two hypothetical proteins of 35.5 Kda and 49.3 Kda, inositol polyphosphate-5-phosphatase, inositol-1,4,5-triphosphate 5-phosphatase type 1, IRAK1, IRAK4, KIAA141, MSTP030, Nek9, PAR3, Pellino 1, Pellino 3, podocalyxin-like protein 1 precursor, Pushover, a putative S-adenosylhomocysteinase, secretory carrier-associated membrane protein 2, surfeit locus protein 2, ubiquitin carboxyl terminal hydrolase 11, upstream regulatory element binding protein 1, Vartul, Werner's syndrome helicase interacting protein (WHIP), X-ray repair cross complementing protein 4 (isoform 1). The present
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                241 KTCKKVAIKIISKRKFAIGSAREADPALNVETBIBILKKLNHPCIIKIKNFFDAED-YYI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           8; Length 543;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 1655.5; DB 8; Length
Pred. No. 1.6e-147;
74; Mismatches 105; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              $
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches 326; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                               sequence represents CHK2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 MSRDTKTESQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 543 AA;
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THAP responsive element; angiogenesis; inflammation; metastasis; cancer; apoptosis; cardiovascular disease; neurodegenerative disease; chemokine; antiangiogenic; antiinflammatory; cardiovascular; cytostatic; neuroprotective; osteopathic; THAP modulator; THAP synthesis modulator; human

Homo sapiens.

WO2004055050-A2

01-JUL-2004.

10-DEC-2003; 2003WO-IB006434

10-DEC-2002; 2002US-0432699P.

(ENDO-) ENDOCUBE SAS. (CNRS) CNRS CENT NAT RECH SCI

Clouaire T; Girard J, Amalric F, Roussigne M,

WPI; 2004-525034/50

N-PSDB; ADQ09233

Modulating expression of a Thanatos (death)-Associated Protein (THAP) responsive gene for preventing or treating e.g. cancer or inflammation, comprises modulating the interaction of a THAP polypeptide with a nucleic

Example 47; SEQ ID NO 417; 612pp; English.

The present invention describes a method for modulating the expression of a thanatos (death)-associated protein (THAP) responsive gene. The method comprises modulating the interaction of a THAP-family polypeptide or its biological freagment with a nucleic acid, and so enhancing or repressing to the expression of the THAP responsive gene. Also described: (1) a method of medulating the expression of a gene responsive to a THAP responsive complex; (2) a pharmaceutical composition comprising a THAP responsive complex; (2) a pharmaceutical carrier; (3) a transcription factor decoy consisting essentially of a THAP responsive element; (4) a cell complexing a virancription factor decoy described above; (5) methods of constraing a virancription factor decoy described above; (5) methods of constructing a viral vector mich comprises a promoter operably linked conducting a viral vector which comprises a promoter operably linked conducting a viral vector which comprises a promoter operably linked conduction of enomeructing a cell which expresses a cell conducting a viral vector which comprises a promoter operably linked conduction and acid encoding a THAP-family polypeptide or its biological fragment, or a mucleic acid and a method of constructing a cell which expresses a cell conduction with a condition mediated by a THAP-femmily polypeptide; (8) a method of amelocating the comprise or its biological test compound that modulates transcription comprises; symptoms associated with a condition mediated by a THAP-femming the analysis or insufficient apoptosis, cardiovascular disease and neurodegenerative comprises; symptoms associated with transcriptional repression or activation comprising a detectable product; (12) a genetically or a chemokine or a THAP-family polypeptide in an individual; or symptoms associated with transcriptional repression or activation comprising a detectable product; (12) a genetically or a middle or its biological fragment; (13) an in vitro transcription comprising the vector described above or that ex composition has antiangiogenic, antiinflammatory, cardiovascular, cytostatic, neuroprotective and osteopathic activities, and can be used as a THAP and THAP synthesis modulator. The composition can be used for modulating the expression of a THAP responsive gene. Modulation us useful for reducing symptoms of conditions us useful angiogenesis, inflammation, metastasis of a cancerous tissue, excessive

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                                                                                                                                                                                                             61 SSLETVSTQELYSIPEDQEPEDQEPEEPTPAPWARLWALQDGFANLECVNDNYWFGRDKS 120
                                                                                                                                                                                                                                                               153 LPLTNNABIALSLPTNKVFVFSDLSVDDQTIYPKDFIDKYIMSRPIGSGACGEVKLAFQK 212
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or insufficient apoptosis, cardiovascular disease or neurodegenerative diseases. The present sequence is used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                  191 RPLNNNSEIALSLSRNKVFVFFFDLTVDDQSVYPKALRDEYIMSKTLGSGACGEVKLAFER
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                                                                                                                                                                                              SSLDTVPVQDLASI----PEDPRIDEDIPQPWGRLWALGKGFLNHDCLHEEYVFGRDKK
                                                                                                                                                                                                                                                CDYTFDIPVLNQTDRYKTYSKRHFRIFQELGHGHSRVANIEDLSGNGTFVNKEIIGKGRT
                                                                                                                                                                                                                                                                                                                                                                      ALEHPWLQDDSMKHTVERLMYGVDHTMPPP---IKKNIIRKRGHEWDQDASTSS-----C
                                                                                                                                           -QSQGTSSSSSSAP-QSYSQSSSSGTL
                                                                                                                                                                                                                                                                                                                                                       213 SVCKKVAVKIISKRKFKMNTSSNEHP-ISVDTEIEILKKLDHPCIIKIENFFDSEDFYYI
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                                                                                                                 Gaps
                                                                                                                 39;
                                                                                      Length 543;
                                                                                     61.0%; Score 1655.5; DB 8; Length 59.9%; Pred. No. 1.6e-147; ive 74; Mismatches 105; Indels
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                                                                                                  Local Similarity ....
                                                                                                                                           2 MSRDTKTESQ-
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                                                            Sequence 543 AA;
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cycle regulatory factor-encoding gene for production recombinant sins with kinase activity, used to develop drugs to treat cancers and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         299 IVLELMEGGELFDKVVGNKRLKEATCKLYFYQMLLAVQYLHENGIIHRDLKPENVLLSSQ 358
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present sequence represents the human cell cycle regulatory factor Cds1. The Cds1 nucleotide sequence can be used in gene therapy. Cds1 may be used to detect inhibitors of cell cycle regulatory factors which can be applied in the development of drugs for treating cancers and proliferative diseases. Cds1 is strongly expressed in the testis as well as other tissues. Cds1 can efficiently phosphorylate cdc25 and histone H1
therapy
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|||| SRESDVEAQQSHGSSACSQPHGSVTQSQGSSSQSQGISSSSTSTMPNS-SQSSHPSSGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       --- QSQGTSSSSSSAPQSYSQSS--SSGT
 gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         41;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          543;
cancer; proliferative disease; cytostatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       60.6%; Score 1643.5; DB 3;
59.6%; Pred. No. 2.2e-146;
ive 75; Mismatches 104; ]
                                                                                                                                                                                                                                                                                                                                                               Claim 1; Page 35-39; 52pp; Japanese.
                                                                                                                           99WO-JP003350.
                                                                                                                                                        98JP-00192467.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity 59.6
Matches 325; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MSRDTKTESQ-----
                                                                                                                                                                                                                                                                                                                                proliferative diseases.
                                                                                                                                                                                        SEIYAKU
                                                                                                                                                                                                                                                    2000-106292/09
 phosphorylation;
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N-PSDB; AAZ57411.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 543 AA;
                                                                                                                                                                                        CHUS CHUGAI
                                                                                                                                                                                                                                                                                                                   proteins with
                                Homo sapiens
                                                           WO9967369-A1
                                                                                                                         23-JUN-1999;
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MSRESDVEAQQSHGSSACSQPHGSVTQSQGSSSQSQGISSSSTSTWPNSSQSSHSSSGTL
                                                                                                                                                                                                                                                                                                                                                                                              SSLDTVPVQDLASI----PEDPEIDEDIPQPWGRLWALGKGFLNHDCLHEEYVFGRDKK
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                                                                                                                                                                                                                                                                                                                                -- OSOGISSSSSSSAP-OSYSOSSSGTL
                                                                                                                                                     The present invention provides the protein and coding sequences of a human Chk2 phosphoensyme inhibitor. The sequences can be used in the chemotherapy of cancers. The present sequence is a protein described the exemplification of the invention
                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 H;
                                                                        New gene encoding a protein for inhibiting human Chk2 phosphoenzyme activity.
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                                                                                                                                                                                                                                                                                                 39;
                                                                                                                                                                                                                                                                     Length 543;
                                                                                                                                                                                                                                                                                                 Indels
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                                                                                                                                                                                                                                                                   DB 5;
                                                                                                                                                                                                                                                                 60.9%; Score 1651.5; DB 5; 59.7%; Pred. No. 3.8e-147; ive 75; Mismatches 105;
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                                                                                                                         Disclosure, Page 27-30, 36pp, Japanese
IGAKU SEIBUTSUGAKU KENKYUSHO
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                                                                                                                                                                                                                                                                                               Matches 325; Conservative
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                                                                                                                                                                                                                                                                                                                                MSRDTKTESO-
                               2002-145186/19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        standard;
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                                            N-PSDB; AAL44751
                                                                                                                                                                                                                                    Sequence 543 AA;
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      Query Match
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antiatreriosclerotic, anticonvulsant, noctropic, neuroprotective, cartionvulsant, noctropic, neuroprotective, cartionvulsant, noctropic, neuroprotective, properties antiallergic, antiinflammatory and thyronimetic activities, and can be used in gene therapy. The human KPP polypeptides and polymcleocides of the invention are useful in diagnosing, treating and preventing diseases or conditions associated with the decreased expression or overexpression of KPP, such as cell proliferative (e.g. cancer, atherosclerosis), neurological (e.g. proliferative (e.g. cancer, atherosclerosis), neurological (e.g. AIDS, allergies) and developmental (e.g. Hypothyroidism, Cushing's syndrome) disorders, or infections. They are also useful in assessing the effects of exogenous compounds on the expression of nucleic acid and amino acid sequences of KPP. The KPP sequences or their fragments are useful in screening compounds for effectiveness as agonist or antagonist of the polypeptides, or in altering the expression of the target polynucleotide and compounds that specifically bind to or modulate the activity of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hafalia AJA, Lee S, Murage J, Swarnakar A, Chawla NK, Khare R;
Elliott VS, Tran UK, Ramkumar J, Gururajan R, Baughn MR, Gietzen KJ;
Yang YG, Chien D, Wang JT, Favero KD, Becha SD, Richardson TW;
Jin P, Hawkins PR, Yue H, Lee EA, Marquis JP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New human kinases and phosphatases (KPP), useful for diagnosing, treating and preventing diseases or conditions associated with the aberrant KPP expression e.g. cancer, AIDS, epilepsy, or infections.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             human; kinase; phosphatase; enzyme; KPP; cytostatic; anticorvulsant; anticorvulsant; noctropic; neuroprotective; cerebroprotective; anticorvulsant; noctropic; neuroprotective; cerebroprotective; anti-HIV; antiallargic; antiinflammatory; thyromimetic; gene therapy; cell proliferative disorder; cancer; atherosclerosis; neurological disorder; epilepsy; Huntington's disease; stroke; immune disorder; inflammatory disorder; AIDS; allergy; developmental disorder; Hypothyroidism; Cushing's syndrome; infection.
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                                                                                                                                                                                                                 ADN61455 standard; protein; 586 AA
                                                                                                                                                                                                                                                                                                                                                                                                      Human KPP-21 protein SEQ ID NO:21.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-NOV-2002; 2002US-0423226P.
15-NOV-2002; 2002US-0426713P.
26-NOV-2002; 2002US-049766P.
11-FEB-2003; 2003US-0447043P.
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                                                                                                                                                                                                                                                                                                                                            12-AUG-2004 (first entry)
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N-PSDB; ADN61511.
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CSEIL 507
                                                          539 CAAVL 543
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503
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Sequence 586 AA;

polypeptide.

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169
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                                                                                                                                                                                                                                                                  170 VFVFSDLSVDDQTIYPKDFIDKYIMSRPIGSGACGEVKLAFQKSVCKKVAVKIISKRKFK 229
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                                                                                                        79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ------CLHEEYVFGRDKKCDYTFDIPVLNQTDRYK
                                                                                                                                                                                                               110 TYSKRHFRIFQELGHGHSRVANIEDLSGNGTFVNKEIIGKGRTLPLTNNAEIALSLPTNK
                                                                                                                                                                                                                                                                                                                      230 MNTSSNEHP-ISVDTEIEILKKLDHPCIIKIENFFDSEDFYYIVLELMEGGELFDRVVNS
                                                                                                                                                                                                                                                                                                                                                                         289 TRLREPIAKLYFYQMLLAVQYLHENGVIHRDLKPENVLLSSTSEECCIKITDFGQSKILG
                                                                                                                                                                                                                                                                                                                                                                                                                             ETSLMRTLCGTPTYLAPEVLNTAGTTGYSSAVDCWSLGVILFVCLCGYPPFSEQNSNIPL
                                                                                                                                                                                                                                                                                                                                                                                                                                            KNOIAEGKYTYIAAAWRNVSEQAFDLVKNILVVDPEQRLTTKQALEHPWLQDDSMKHTVE
                                                     -----QSQGTSSSSSSAP-QSYSQSSSGTL
                                                                             1 MSRESDVEAQQSHGSSACSQPHGSVTQSQGSSSQGSSSSSTSTMPNSSQSSHSSSGTL
                           Gaps
                           82;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 586;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   469 RLMYGVDHTMPPP---IKKNIIRKRGHEWDQDASTSS-----CSEIL 507
                                                                                                       38 SSLDTVPVQDLASI-----PEDPEIDEDIPQPWGRLWALGKGFLNHD-
59.9%; Score 1624; DB 8; Length 55.5%; Pred. No. 1.7e-144; ive 74; Mismatches 105; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human; Chk2 phosphoenzyme inhibitor; cytostatic.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human Chk2 phosphoenzyme inhibitor.
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                                                    2 MSRDTKTESQ-----
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                          Conservative
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N-PSDB; AAL44749.
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CDYTFDIPVLNQTDRYKTYSKRHFRIFQELGHGHSRVANIEDLSGNGTFVNKEIIGKGRT 152
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            332 EECCIKITDFGQSKILGETSLMRTLCGTPTYLAPEVLNTAGTTGYSSAVDCWSLGVILFV 391
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ----IIDEGHSKILGETSLMRTLCGTPTYLAPEVLVSVGTAGYNRAVDCWSLGVILFI 390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLCGYPPFSEQNSNIPLKNQIAEGKYTYIAAAMRNVSEQAFDLVKNLLVVDPEQRLTTKQ 451
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ALEHPWLQDDSMKHTVERLMYGVDHTMPPP---IKKNIIRKRGHEWDQDASTSS----C 503
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  detection; cancer; 8q22.3; chromosome 8; human; EDD; tumour suppressor; cell cycle modulator; DNA repair; DNA damage; nuclear targeting protein; progesterone receptor; cytostatic; gene therapy; squamous cell carcinoma; hepatocellular carcinoma; ovarian cancer; breast cancer; melanoma; head and neck cancer; adenocarcinoma; squamous lung cancer; adenocarcinoma; squamous lung cancer; gastrointestinal cancer; renal cell cancer; bladder cancer;
                                                                                                                                                                                                                                                                                                   9
                                                                                                                                                                                                                                                                                                                                    SSLDTVPVQDLASI----PEDPEIDEDIPQPWGRLWALGKGFLNHDCLHEEYVFGRDKK 92
                                                                                                                                                                                                                                                                                        -----QSOCISSSSSSAP-QSYSQSSSGTL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SVCKKVAVKIISKRKFKMNTSSNEHP-ISVDTEIEILKKLDHPCIIKIENFFDSEDFYYI
                                                                                                                                                                                                                                      Gaps
                                                                              The present invention provides the protein and coding sequences of a human Chk2 phosphoenzyme inhibitor. The sequences can be used in the chemotherapy of cancers. The present sequence is the protein of the
encoding a protein for inhibiting human Chk2 phosphoenzyme
                                                                                                                                                                                                                                      68;
                                                                                                                                                                                                   55.3%; Score 1499; DB 5; Length 514;
                                                                                                                                                                                                                 55.5%; Pred. No. 1e-132;
ive 72; Mismatches 102; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human Chk2 transcript variant 2 protein SEQ ID NO:21.
                                               Claim 2; Page 13-16; 36pp; Japanese
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADL32563 standard; protein; 514 AA
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Matches 302; Conservative
                                                                                                                                                                                                                                                                   2 MSRDTKTESQ-----
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                                                                                                                                                                   Sequence 514 AA;
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                                                                                                                                  invention
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                                                                                                                                                                                                 Query Match
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The present invention describes a method for detecting a cancer cell in a subject, which comprises determining the level of nucleic acid that is liked to map position 8q23.3 of the human genome or its expression product in a sample of the subject, where an elevated level of the product in a sample of the subject, where an elevated level of the product in a sample of the subject, where an elevated level of the comprision of a cancer in a subject comprising a cancer or predicting recurrence of a cancer in a subject comprising determining the level of mRNA or protein encoded by a nucleic acid as described above; (2) the isolated or nucleic acid molecule for detecting cancer cell; (3) an isolated or recombinant protein complex; (4) an antibody that binds to the protein complex; (5) a kit for detecting or producing a protein mount suppression comprising an EDD polypeptide or a portion of an EDD polypeptide or a portion of an EDD polypeptide or a portion of an EDD polypeptide or a portion, where the portion of the second polypeptide sletting the portion, where the portion of the second polypeptide is sufficient to bind to the EDD polypeptide or the portion of an EDD polypeptide; (6) methods for isolating the protein complex; (7) a method for determining a predisposition for disease, or disease state; (8) a method for determining a modulator of the level of protein complex; (7) a method for treating a condition sociated with a cancer, (8) and the complex of the level of protein complex; (10) a method for treating a condition sociated with a cancer, (9) a condition of the level of protein complex; (11) an antisense nucleic acid, ribozyme, peptide nucleic acid (RNA), interfering RNA or siRNA; and (11) a pharmaceutical composition comprising the antisense nucleic acid, ribozyme, peptide nucleic acid (RNA), interfering a condition a septiated with EDD box cancer; adenoment sequence of the method for creating a condition a septiated with EDD box cancer; adenoment of the acid, ribozyme, peptide moder of the sequence of the 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     lung cancer, gastrointestinal cancer (e.g. gastric, colon, or pancreatic cancer), renal cell cancer, bladder cancer, prostate cancer, non-squamous carcinoma, glioblastoma and medullablastoma. The components and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                composition are useful for reducing the expression of EDD in a cell to inhibit cellular proliferation. The present sequence represents human Chk2 transcript variant 2 protein, which is used in the exemplification
prostate cancer; non-squamous carcinoma; glioblastoma; medullablastoma; Chk2 transcript variant 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Detecting a cancer cell in a subject sample, also related to cancer treatments, comprises determining the level of nucleic acid that is linked to map position 8q22.3 of the human genome or its expression
                                                                                                                                                                                                                                                                                                                                                                                                      Henderson M, Clancy J, Henshall S;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 29; SEQ ID NO 21; 331pp; English.
                                                                                                                                                                                                                                                                                                                                                     (GARV-) GARVAN INST MEDICAL RES
                                                                                                                                                                                                                                                                          05-SEP-2002; 2002AU-00951346.
07-NOV-2002; 2002US-0425218P.
                                                                                                                                                                                                                           05-SEP-2003; 2003WO-AU001164
                                                                                                                                                                                                                                                                                                                                                                                                   Watts C, Saunders D, Hei
Sutherland R, O'brien P;
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                                                                             Homo sapiens.
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Gaps

68;

55.3%; Score 1499; DB 8; Length 514; 55.5%; Pred. No. 1e-132; ive 72; Mismatches 102; Indels 68

Conservative

Best Local Similarity Matches 302; Conserv

Query Match

Sequence 514 AA;

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61 SSLETVSTQELYSIPEDQEPEDQEPEEPAPWARLWALQDGFANLECVNDNYWFGRDKS 120
                                            272 VLELMEGGELFDRVVNSTRLREPIAKLYFYQMLLAVQYLHENGVIHRDLKPENVLLSSTS 331
                                                                                                                        332 EECCIKITDFGQSKILGETSLMRTLCGTPTYLAPEVLNTAGTTGYSSAVDCWSLGVILFV 391
                                                                                                                                               ALEHPWLODDSWKHTVERLMYGVDHTMPPP---IKKNIIRKRGHEWDQDASTSS----C 503
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                      SSLDTVPVQDLASI ---- PEDPEIDEDIPQPWGRLWALGKGFLNHDCLHEEYVFGRDKK 92
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Search completed: July 7, 2005, 12:59:10 Job time : 166 secs

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Sequence 2, Appli Sequence 5, Appli Sequence 5, Appli Sequence 4, Appli

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Publication No. US2020086392A1

GENERAL INFORMATION:

APPLICANT: CALIFORNIA INSTITUTE OF TECHNOLOGY

APPLICANT: GUO, Zijan

TITLE OF INVENTION: CHECKPOINT-ACTIVATING OLIGONUCLEOTIDES

FILE REFERENCE: CIT1350-1

CURRENT APPLICATION NUMBER: US/09/849,617

CURRENT APPLICATION NUMBER: US 60/202,028

PRIOR PILING DATE: 2000-05-04

NUMBER OF SEQ ID NOS: 14

SOFTWARE: PatentIn version 3.0

LENGTH: 517
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100.0%; Pred. No. 3.5e-193;
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Best Local Similarity 100.
Matches 517; Conservative
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US-10-185-182A-2

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US-10-180-187-17-2

US-10-180-180-17-1

US-10-142-356-6

US-09-740-627-1

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Maximum Match 100%
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                    TYLAPEVLNTAGTTGYSSAVDCWSLGVILFVCLCGYPPFSEQNSNIPLKNQIAEGKYTYI
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Sequence 2, Application US/20030017160A1

GENERAL INFORMATION

APPLICANT: LUYTEN, Walter H.M.L.

APPLICANT: MCGONAN, Clare H.

APPLICANT: MCGONAN, Clare H.

APPLICANT: BLASINA, Clare H.

APPLICANT: BLASINA, Clare H.

APPLICANT: BLASINA, Clare H.

CURENT FILLO OF INVENTION: COMPOSITIONS AND METHODS

TITLE OF INVENTION: COMPOSITIONS AND METHODS

TURRENT APPLICATION NUMBER: US/10/185,182A

CURRENT PILLING DATE: 2002-09-04

PRIOR FILLING DATE: 2000-04-07

PRIOR APPLICATION NUMBER: PCT/EP98/06981

PRIOR APPLICATION NUMBER: PCT/EP98/06981

PRIOR APPLICATION NUMBER: GB 9722320.0

PRIOR FILING DATE: 1998-10-21

PRIOR FILING DATE: 1997-10-22

NUMBER OF SEQ ID NOS: 6

SOFTWARKE: FastSEQ for Windowe Version 4.0
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Matches 326; Conservative
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ORGANISM: Homo Sapiens
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                                                                                                    QTIYPKDF1DKYIMSRP1GSGACGEVKLAFQKSVCKKVAVKIISKRKFKMYSSNEHPIS
                                                                                                                                                                                 241 VDTEIEILKKLDHPCIIKIENFFDSEDFYYIVLELMEGGELFDRVVNSTRLREPIAKLYF
                                                                                                                                                                                                                                                                301 YQMLLAVQYLHENGVIHRDLKPENVLLSSTSEECCIKITDFGGSKILGETSLMRTLCGTP
                                                                                                                                                                                                                                                                                                                      TYLAPEVLMTAGTTGYSSAVDCWSLGVILFVCLCGYPPFSEQNSNIPLKNOIAEGKYTYI
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  ELGHGHSRVANIEDLSGNGTFVNKEIIGKGRTLPLTNNAEIALSLPTNKVFVFSDLSVDD
                         ELGHGHSRVANIEDLSGNGTFVNKEIIGKGRTLPLTNNAEIALSLPTNKVFVFSDLSVDD
                                                                               QTIYPKDFIDKYIMSRPIGSGACGEVKLAFQKSVCKKVAVKIISKRKFKMNTSSNEHPIS
                                                                                                                                                            VDTEIEILKKLDHPCIIKIENFFDSEDFYYIVLELMEGGELFDRVVNSTRLREPIAKLYF
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                                                                                                                                                                                                                                         YOMLLAVQYLHENGVIHRDLKPENVLLSSTSEECCIKITDFGQSKILGETSLMRTLCGTP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 2, Application US/10618173
; Publication No US20040018603A1
; GENERAL INKORMATION:
; APPLICANT: CALIFORNIA INSTITUTE OF TECHNOLOGY
; APPLICANT: GUO, Zijian
; APPLICANT: GUO, Zijian
; APPLICANT: GUO, Zijian
; TILLE OF INVENTION: CHECKPOINT-ACTIVATING OLIGONUCLEOTIDES
; FILE REFERENCE: CITTI350-1
; CURRENT APPLICATION NUMBER: US/09/849,617
; PRIOR PILING DATE: 2001-09-17
; PRIOR APPLICATION NUMBER: US 60/202,028
; PRIOR FILING DATE: 2001-09-17
; PRIOR FILING DATE: 2000-05-04
; NUMBER OF SEQ ID NOS: 14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PIKKNIIRKRGHEWDODASTSSCSEILPTSAEKRAKR
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Best Local Similarity
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420 CLSGYPPFSEHRTQVSLKDQITSGKYNFIPEVWAEVSEKALDLVKKLLVVDPKARFTTEE 479
                                                                                                                                                                                                                                                               61 SSLETVSTQELYSIPEDQEPEDQEPEEPTPAPWARLWALQDGFANLECVNDNYWFGRDKS 120
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VLELMEGGELFDKVVCNKRLKEATCKLYFYQMLLAVQYLHENGIIHRDLKPENVLLSSQE 359
                                                                                                                                                      CLCGYPPFSEQNSNIPLKNQIAEGKYTYIAAAWRNVSEQAFDLVKNLLVVDPEQRLTTKQ 451
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                                                                 EECCIKITDFGQSKILGETSLMRTLCGTPTYLAPEVLNTAGTTGYSSAVDCWSLGVILFV
                                                                                                                                                                                                                                       ALEHPWLQDDSMKHTVERLMYGVDHTMPPP---IKKNIIRKRGHEWDQDASTSS----C
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59.9%; Pred. No. 1.5e-114;
ive 74; Mismatches 105; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 2, Application US/10820583A
Publication No. US20040242461A1
GENERAL INFORMATION:
APPLICANT: Schneider, Michael
APPLICANT: Schneider, Michael
TITLE OF INVENTION: Modulators of Telomere Stability
FILE REFERENCE: HO-P02671W51
CURRENT FILING DATE: 2004-04-08
FRIOR FILING DATE: 2003-04-08
FRIOR FILING DATE: 2003-04-08
FRIOR FILING DATE: 2003-04-08
FRIOR FILING DATE: 2003-04-08
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Best Local Similarity 59.99
Matches 326; Conservative
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ORGANISM: Human
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US-10-820-583A-2
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APPLICANT: Trancis Recuesing
APPLICANT: Trancis Roussigne
APPLICANT: Thomas Cloudire
TITLE OF INVENTION: THAP PROTEINS AS NUCLEAR RECEPTORS FOR
TITLE OF INVENTION: CHEMOKINES AND ROLES IN TRANSCRIPTIONAL REGULATION,
TITLE OF INVENTION: PROLIFERATION AND CELL DIFFERENTIATION
TITLE OF INVENTION: PROLIFERATION AND CELL DIFFERENTIATION
CURRENT APPLICATION NUMBER: US/10/733,878
CURRENT APPLICATION NUMBER: 06/432699
PRIOR FILING DATE: 2002-12-10
PRIOR FILING DATE: 2003-07-03
NUMBER OF SEQ ID NOS: 535
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               240
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  VLELMEGGELFDRVVNSTRLREPIAKLYFYQMLLAVQYLHENGVIHRDLKPENVLLSSTS 331
                      300 VLELMEGGELFDKVVGNKRLKEATCKLYFYQMLLAVQYLHENGIIHRDLKPENVLLSSQE 359
                                                                                     EECCIKITDFGQSKILGETSLMRTLCGTPTYLAPEVLNTAGTTGYSSAVDCWSLGVILFV 391
                                                                                                             360 EDCLIKITDFGHSKILGETSLMRTLCGTPTYLAPEVLVSVGTAGYNRAVDCWSLGVILFI 419
                                                                                                                                                                          CLCGYPPFSEQNSNIPLKNQIAEGKYTYIAAAWRNVSEQAFDLVKNLLVVDPEQRLTTKQ 451
                                                                                                                                                                                                ALEHPWLQDDSMKHTVERLMYGVDHTMPPP---IKKNIIRKRGHEWDQDASTSS----C 503
                                                                                                                                                                                                                                                                                      CDYTFDIPVLNQTDRYKTYSKRHFRIFQELGHGHSRVANIEDLSGNGTFVNKEIIGKGRT 152
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| MSRESDVEAQQSHGSSACSQPHGSVTQSQGSSSQĞQISSSSTSTMPNSSQŠSHSSSĞTL
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Publication No. US20040224408A1
GENERAL INFORMATION:
APPLICANT: Jean-Philippe Girard
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Francois Amalric
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches 326; Conservative
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                504 SEIL 507
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US-10-733-878-417
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RESULT 8
US-10-820-583A-3
Sequence 3, Application US/10820583A
Publication No. US20040242461A1
                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 59.6
Matches 325; Conservative
                                                                                                                                                                                                                                                                                                                                                                                          2 MSRDTKTESQ-----
                                                                                                                                                                                                                                                                               TYPE: PRT
ORGANISM: Homo sapiens
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CLCGYPPFSEQNSNIPLKNQIAEGKYTYIAAAWRNVSEQAFDLVKNLLVVDPEQRLTTKQ 451
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                                                     ALEHPWLQDDSMKHTVERLMYGVDHTMPPP---IKKNIIRKRGHEWDQDASTSS----C
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                                                                                                                                                                                                                                              APPLICANT: Boylan, John F.
APPLICANT: Bowers, Alex J.
TITLE OF INVENTION: Serine-Threonine Kinase Member, h2520-40
TITLE OF INVENTION: Serine-Threonine Kinase Member, h2520-40
FILE REFERENCE: 01017/3717A
CURRENT FILING DATE: 2002-05-09
PRIOR PILING DATE: 2002-05-09
PRIOR PILING DATE: 2001-05-10
NUMBER OF SEQ ID NOS: 23
SOFTWARE: Patentin version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          60.6%; Score 1644.5; DB 14; Length 63.0%; Pred. No. 9.8e-114; Live 69; Mismatches 108; Indels
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                                                                                                                                                                                                        Sequence 6, Application US/10142356 Publication No. US20030036183A1 GENERAL INFORMATION:
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Best Local Similarity 63.0%
Matches 327; Conservative
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                                                                                                            504 SEIL 507
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59.6%; Pred. No. 1.2e-113;
cive 75; Mismatches 104; Indels
                                                          APPLICATION TOWNS AND THE APPLICATION TO THE OF INVENTION: CELL CYCLE REGULATING FACTOR FILE REFERENCE: 06501-071001
CURRENT APPLICATION NUMBER: US/09/740,627
CURRENT FILING DATE: 2000-12-19
PRIOR APPLICATION NUMBER: PCT/JP99/03350
PRIOR APPLICATION NUMBER: DP 10/192467
PRIOR PLING DATE: 1999-06-23
NUMBER OF SEQ ID NOS: 11
SOFTWARE: FastSEQ for Windows Version 4.0
; Sequence 1, Application US/09740627; Patent No. US20020012964A1; GENERAL INFORMATION:
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LENGTH: 326
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Publication No. US20050112746A1
GENERAL INFORMATION:
APPLICANT: Structural GenomiX, Inc.
APPLICANT: Antonysamy, Stephen S.
APPLICANT: Hendle, Jorg
APPLICANT: Louis, Gordon V.
TITLE OF INVENTION: Crystals and Structures of Protein Kinase CHK2
FILE REFERENCE: 022132-001210US
                                                                                                                                                                                                                                                                                           68;
                                                                                                                                                                                                                                                             DB 16; Length 514;
                                                                                                                                                                                                                                                             ; Score 1499; DB 16; Length 5; Pred. No. 6e-103; 72; Mismatches 102; Indels
APPLICANT: Schneider, Michael
APPLICANT: Schneider, Michael
APPLICANT: Oh, Hidemasa
TITLE OF INVENTION: Modulators of Telomere Stability
FILE REPERENCE: HO-PO2673US1
CURRENT APPLICATION NUMBER: US/10/820,583A
CURRENT FILING DATE: 2004-04-08
PRIOR PILLING DATE: 2003-04-08
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                                                                                                                              NUMBER OF SEQ ID NOS: 24
SOFTWARE: PatentIn version 3.1
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Best Local Similarity 55.5
Matches 302; Conservative
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ORGANISM: Human
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US-10-881-124A-9
                                                                                                                                                            SEQ ID NO 3
LENGTH: 514
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APPLICANT: Structural Genomix, Inc.
APPLICANT: Antonysamy, Stephen S.
APPLICANT: Antonysamy, Stephen S.
APPLICANT: Hendle, Jorg
APPLICANT: Hendle, Jorg
APPLICANT: House, Gordon V.
TITLE OF INVENTION: Crystals and Structures of Protein Kinase CHK2
FILE REPERRORS: 02102100US
CURRENT FILING DATE: 2004-06-30
PRIOR APPLICATION NUMBER: US 60/484,389
PRIOR FILING DATE: 2003-07-01
PRIOR FILING DATE: 2003-07-01
PRIOR FILING DATE: 2003-07-01
PRIOR FILING DATE: 2003-07-01
NUMBER OF SEQ ID NOS: 14
SOFTWARE: Patentin Version 3.1
SEQ ID NO 8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 40.4%; Score 1096.5; DB 17; Length 326; Best Local Similarity 64.8%; Pred. No. 3e-73; Matches 210; Conservative 43; Mismatches 66; Indels 5;
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CURRENT APPLICATION NUMBER: US/10/881,124A;
CURRENT FILING DATE: 2004-06-30
PRIOR APPLICATION NUMBER: US 60/484,389
FRIOR FILING DATE: 2003-07-01
PRIOR FILING DATE: 2003-07-01
PRIOR FILING DATE: 2003-10-08
NUMBER OF SEQ ID NOS: 14
SEQ ID NO 9
SEQ ID NO 9
                                                                                                                                                                                                                                                                                                                                                                                                        ; OTHER INFORMATION: Synthetic construct US-10-881-124A-9
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Sequence 1578, Application US/10169493
Fublication No. US20030233675A1
GENERAL INFORMATION:
APPLICANT: Cao, Yongwei
APPLICANT: Galdman, Barry S.
APPLICANT: Goldman, Barry S.
APPLICANT: Goldman, Barry S.
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF TITLE OF INVENTION: UNMBER: US/10/369,493
CURRENT APPLICATION NUMBER: US/10/369,493
CURRENT FILING DATE: 2003-02-28
PRIOR APPLICATION NUMBER: US 60/360,039
PRIOR FILING DATE: 2002-02-28
PRIOR APPLICATION NUMBER: US 60/360,039
NUMBER OF SEQ ID NOS: 47374
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345 SQVQLGPWDEDEIDIQVKIADFGLAKFTGEMQFTNTLCGTPSYVAPEVLT---KKGYTSK 401
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    236 -EHPISVDTEIEILKKLDHPCIIKIENFFDSEDFYYIVLELMEGGELFDRVVNSTRLREP
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; ORGANISM: Saccharomyces cerevisiae
US-10-369-493-1578
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                                                                                                  DB 17; Length 327;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 9, Application US/09740627
Patent No. US20020012964A1
GENERAL INFORMATION:
TITLE OF INVENTION: CELL CYCLE REGULATING FACTOR
FILE REFERENCE: 06501-071001
CURRENT FILING DATE: 2000-12-19
PRIOR APPLICATION NUMBER: US/09/740,627
CURRENT FILING DATE: 1999-06-23
PRIOR PLICATION NUMBER: US/09/0350
PRIOR PLICATION NUMBER: US/099/03350
PRIOR FILING DATE: 1999-06-23
PRIOR FILING DATE: 1999-06-23
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NOS: 11
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                             40.4%; Score 1096.5; DE 64.8%; Pred. No. 3e-73; ive 43; Mismatches 6
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                                                                                                                                                                                      Conservative
                                                                                                                                     Local Similarity
JS-10-881-124A-8
                                                                                                                                                                                 Watches 210;
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US-09-740-627-9
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258 KIENFFDSEDFYYIVLELMEGGELFDRVVNSTRLREPIAKLYFYQMLLAVQYLHENGVIH 317
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                           APPLICANT: Zambrowicz, Brian
APPLICANT: Zambrowicz, Brian
APPLICANT: Abuin, Alejandro
APPLICANT: Abuin, Alejandro
APPLICANT: Sands, Arthur T.
TITLE OF INVENTION: No. US20040014112Alel Human Kinase Proteins and
TITLE OF INVENTION: Polynucleotides Encoding the Same
FILE REFERENCE: LEX-0103-USA
CURRENT APPLICATION NUMBER: US/10/446,175
CURRENT FILING DATE: 2000-12-07
PRIOR APPLICATION NUMBER: US/09/733,388
PRIOR FILING DATE: 1999-12-07
PRIOR FILING DATE: 1999-12-07
NUMBER OF SEQ ID NOS: 5
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 4
LENGTH: 356
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Publication No. US20050079530A1

GENERAL INFORMATION:
APPLICANT: Scoville, John
APPLICANT: Turner, C. Alexander Jr.
APPLICANT: Triedrich, Glenn
APPLICANT: Eriedrich, Glenn
APPLICANT: Sands, Arthur T.
TITLE OF INVENTION: Novel Human Kinase Proteins and
TITLE OF INVENTION: Polynucleotides Encoding the Same
TITLE OF INVENTION: Polynucleotides Encoding the Same
TITLE OF INVENTION: OPINUCLEUS CONTROLLY CONTROLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 22.2%; Score 603; DB 15; Sest Local Similarity 38.1%; Pred. No. 1.7e-36; Matches 128; Conservative 62; Mismatches 106;
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CURRENT FILING DATE: 2004-09-08
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PRIOR PAPPLACATION NUMBER: US/10/446,175
PRIOR FILING DATE: 2003-05-27
PRIOR APPLICATION NUMBER: US/09/733,388
PRIOR FILING DATE: 2000-12-07
PRIOR PRILOR APPLICATION NUMBER: US 60/169,428
PRIOR FILING DATE: 1999-12-07
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ORGANISM: Homo sapiens
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US-10-936-445-4
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                                   198 IGSGACGEVKLAFQKSVCKKVAVKIISKRKFKMNTSSNEHPISVDTEIEILKKLDHPCII 257
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; Bublication No. US20030064495A1
; GENERAL INFORMATION:
; APPLICANT: Donoho, Greg
; APPLICANT: Turner, C. Alexander Jr.
; APPLICANT: Abuin, Alejandro
; APPLICANT: Sands, Arthur T.
; TITLE OF INVENTION: Polynucleotides Encoding the Same
; TITLE OF INVENTION: Polynucleotides Encoding the Same
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309 FNATAVVRHMRKLHLGSSLDSSNASVSSSLSLASQK 344
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CURRENT FILING DATE: 2000-12-07
PRIOR PILING DATE: 1999-12-07
NUMBER OF SEQ ID NOS: 5
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 4
LENGTH: 356
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APPLICANT: Donoho, Greg
APPLICANT: Scoville, John
APPLICANT: Turner, C. Alexander Jr.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 38.13
Matches 128; Conservative
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US-10-446-175-4
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438 LLVVDPEQRLTTKQALEHPWLQDDSMKHTVERLMYGVDHTMPPPIKKNIIRKRGHEWDQ- 496
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                                                                                                                                          Gaps
                                                                                   Query Match
22.2%; Score 603; DB 17; Length 356;
Best Local Similarity 38.1%; Pred. No. 1.7e-36;
Matches 128; Conservative 62; Mismatches 106; Indels 40;
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; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 356
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-936-445-4
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Sequence 1078, A
Sequence 4, Appli
Sequence 10, Appli
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Sequence 7461, Ap
Sequence 7462, Ap
Sequence 2, Appli
Sequence 17, Appli
                                                                                                                                                          7, 2005, 12:50:39 ; Search time 43 Seconds (without alignments) 897.525 Million cell updates/sec
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/cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
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/cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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US-09-529-152-1
US-09-529-154-2
US-09-733-388-4
US-10-446-175-4
US-10-55-975-641-10
US-09-733-388-2
US-10-446-175-4
US-10-55-975A-10
US-09-733-388-2
US-10-446-175-2
US-09-733-388-2
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Sequence 4, Appli Sequence 4, Appli Sequence 4, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 6544, Ap Sequence 6544, Ap Sequence 6, Appli Sequence 2, Appli Sequence 18494, Appli Sequence 18494, Appli Sequence 18494, Appli	IDES		LUIVEVQULASIFEDEEIDED 60 PVLNQTDRYKTYSKRHPRIFQ 120 PVLNQTDRYKTYSKRHPRIFQ 120	
US-09-992-481-4 US-10-434-0134-4 US-09-975-326-4 US-09-975-326-2 US-10-217-357-2 US-09-949-016-6544 US-09-949-016-6544 US-09-633-3288-4 US-09-633-3288-2 US-09-633-3288-2 US-09-633-3288-2 US-09-633-3288-2 US-09-633-3288-2 US-09-633-3288-2 US-09-633-3288-2 US-09-272-796-5 US-09-272-796-5 US-09-272-796-5 US-09-272-796-5 US-09-272-796-5 US-09-278-796-5 US-09-278-796-5 US-09-278-796-7 US-09-278-796-7 US-09-278-796-7 US-09-278-796-7	ALIGN 7 7 TIVAT 7/849,	; Score 2712; DB 4; ; Pred. No. 2e-254; 0; Mismatches 0; SSSSSAPQSYSQSSSGTLSSLD	MMSKDIKIESQQSQGISSSSSSSSAPQSISSSSGILSSLDIVEVQDLASSLEDE IPOPWGRLWALGKGFLNHDCLHEEVVEGRDKKCDYTFDIPVLNQTDRYKTYSKRHFRIF	ELGHGHSRVANIEDLSGNGTFVNKEIIGKGRTLPLTNNAEIALSLPTNKVFVFSDLSVDD
19.1 19.1 18.5 18.5 18.5 18.5 18.5 18.5 18.3 18.3 18.3 18.3 18.3 18.3 18.3 18.0 19.0	4 HU 4 45005 4	100.0% Similarity 100.0% 17; Conservative MMSRDTKTESQOSQGTSS(MMSKUTKTESQQSQGTSSS IPQPWGRLWALGKGFLNHI IPQPWGRLWALGKGFLNHI IPQPWGRLWALGKGFLNHI	ELGHGHSRVANIEDLSGN(
28 29 30 31 31 31 32 31 33 34 496 496 496 496 496 496 496 49	RESULT 1 US-09-849-617-2 Sequence 2, Application Sequence 2, Application GENERAL INFORMATION: APPLICANT: CALIFORNIA APPLICANT: CALIFORNIA APPLICANT: DUNEHY, WI TITLE OF INVENTION: CI FILE REFERENCE: CIT13 CURRENT APPLICATION NUM CURRENT APPLICATION NUM FRICH APPLICATION NUM CURRENT APPLICATION NUM CURRENT APPLICATION NUM PRIOR APPLICATION NUM SEQ ID NOS: SOFTWARE: PATENT NUMBER OF SEQ ID NOS: SEQ ID NOS: SEQ ID NOS: LENGTH: S17 TYPE: PRT CREATER FOR SEX IN NOS: SEQ ID NOS: SEQ IN N	Query Match Best Local S Matches 517	20 61 E1	Qy 121 Db 121 Qy 181 Db 181
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RESULT 3
US-09-529-154-2
i Sequence 2, Application US/09529154
j Patent No. 6531312
i GENERAL INFORMATION:
j APPLICANT: LUYTEN, Malter H.M.L.
j APPLICANT: LUYTEN, Malter H.M.L.
j APPLICANT: LUYTEN, Malter H.M.L.
j TITLE OF INVENTION: A NOVEL HUMAN CHECKPOINT KINASE, hCDS1, COMPOSITIONS
j TITLE OF INVENTION: AND METHODS
j FILE REFERENCE: JAB 133 (US)
j CURRENT PILING DATE: 200-04-07
j PRIOR APPLICATION NUMBER: US/09/529,154
j PRIOR APPLICATION NUMBER: GB 9722320.0
j PRIOR PILING DATE: 1997-10-22
j NUMBER OF SEQ ID NOS: 6
j SOFTWARE: PATENTIN VET: 2.0
j SEQ ID NO 2
j LENGTH: 543
                                                 539
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Patent No. 6413755

GENERAL INFORMATION

APPLICANT: LOTTEN, Walter H.M.L.

APPLICANT: PARKER, Andrew E.

APPLICANT: MCGOWAN, Clare H.

APPLICANT: BLASINA, Alessandra

TITLE OF INVENTION: Human Checkpoint Kinase, hCDS1, Compositions and Methods

TITLE OF INVENTION: Human Checkpoint Kinase, hCDS1, Compositions and Methods

CURRENT APPLICATION NUMBER: US/09/529,093A

CURRENT PILING DATE: 1908-10-21

PRIOR APPLICATION NUMBER: GB 9722320.0

PRIOR FILING DATE: 1997-10-22

NUMBER OF SEQ ID NOS: 6

SOFTWARE: Patentin Ver. 2.0
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                                                                              61 SSLETVSTQELYSIPEDQEPEDQEPEEPTPAPWARLWALQDGFANLECVNDNYWFGRDKS 120
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                   361 TYLAPEVLNTAGTTGYSSAVDCWSLGVILFVCLCGYPPFSEQNSNIPLKNOIAEGKYTYI
                                                              AAAWRNVSEQAFDLVKNLLVVDPEQRLTTKQALEHPWLQDDSMKHTVERLMYGVDHTMPP
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 TYLAPEVLNTAGTTGYSSAVDCWSLGVILFVCLCGYPPFSEONSNIPLKNOIAEGKYTYI
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                                                                                                                                              PIKKNIIRKRGHEWDQDASTSSCSEILPTSAEKRAKR 517
                                                                                                                          PIKKNIIRKRGHEWDQDASTSSCSEILPTSAEKRAKR 517
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59.9%;
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Best Local Similarity 59.9
Matches 326; Conservative
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ORGANISM: Homo sapiens
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LENGTH: 356
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                                                                                                                                Sequence 10788, Application US/09949016

| Sequence 10788, Application US/09949016
| Patent No. 6812339
| GENERAL INFORMATION:
| APPLICANT: VEXTER, J. Craig et al.
| APPLICANT: VEXTER, J. Craig et al.
| TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;
| TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;
| CURRENT APPLICATION NUMBER: US/09/949, 016
| CURRENT APPLICATION NUMBER: 60/241, 755
| PRIOR FILING DATE: 2000-10-20
| PRIOR APPLICATION NUMBER: 60/231, 768
| PRIOR APPLICATION NUMBER: 60/231, 498
| PRIOR FILING DATE: 2000-10-03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          153 LPLTNNAEIALSLPTNKVFVFSDLSVDDQTIYPKDFIDKYIMSRPIGSGACGEVKLAFQK 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  213 SVCKKVAVKIISKRKFKMNTSSNEHP-ISVDTEIEILKKLDHPCIIKIENFFDSEDFYYI 271
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    392 CLCGYPPFSEQNSNIPLKNQIAEGKYTYIAAAWRNVSEQAFDLVKNLLVVDPEQRLTTKQ 451
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   58.6%; Score 1589.5; DB 4; Length 64.0%; Pred. No. 2e-145; ive 60; Mismatches 83; Indels
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Best Local Similarity 64.0°
Matches 310, Conservative
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504 SEIL 507
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US-09-949-016-10788
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US-09-949-016-10788
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RESULT

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143 RDLKPENLLYYSQDEESKIMISDFGLSKWEGKGDVMSTACGTPGYVAPEVL---AQKPYS 199
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APPLICANT: Donoho, Greg
APPLICANT: Scoville, John
APPLICANT: Turner, C. Alexander Jr.
APPLICANT: Turner, C. Alexander Jr.
APPLICANT: Zambrowicz, Brian
APPLICANT: Abuin, Alejandro
APPLICANT: Sands, Arthur T.
TITLE OF INVENTION: No. 6602698el Human Kinase Proteins and
TITLE OF INVENTION: Polymucleotides Encoding the Same
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APPLICANT: Abuin, Alejandro
APPLICANT: Sands, Arthur T.
IITLE OF INVENTION: 06. 6806673el Human Kinase Proteins and
TITLE OF INVENTION: Polynucleotides Encoding the Same
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                                                                                                                                                                                                                                                                               FILE REFERENCE: LEX-0103-USA
CURRENT APPLICATION NUMBER: US/09/733,388
CURRENT FILING DATE: 2000-12-07
PRIOR APPLICATION NUMBER: US 60/169,428
PRIOR FILING DATE: 1999-12-07
NUMBER OF SEQ ID NOS: 5
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 4
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CURRENT APPLICATION NUMBER: US/10/446,175
CURRENT FILING DATE: 2003-05-27
PRIOR APPLICATION NUMBER: US/09/733,388
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APPLICANT: Scoville, John
APPLICANT: Turner, C. Alexander Jr.
APPLICANT: Friedrich, Glenn
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Patent No. 6806073
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Matches 128; Conservative
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ORGANISM: Homo sapiens
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RDLKPENVLLSSTSEECCIKITDFGQSKILGETSLMRTLCGTPTYLAPEVLNTAGTTGYS 377
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APPLICANT: Immunex Corporation
APPLICANT: Bird, Timothy A.
APPLICANT: Virca, G. Duke
APPLICANT: Marcin, Unja
APPLICANT: Maderson, Dirk M.
ITILE OF INVENTION: CALCIUM/CALMODULIN-DEPENDENT KINASE
FILE REPERENCE: 2923-B
CURRENT APPLICATION NUMBER: US/10/355,975A
CURRENT APPLICATION NUMBER: US/10/355,975A
SOFTWARE: Patentin version 3.1
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310 FNATAVVRHMRRLQLGSSLDSSNASVSSNLSLASQK 345
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310 FNATAVVRHMRRLQLGSSLDSSNASVSSNLSLASQK 345
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                                                                                                                                                                                                                          Query Match 22.1%; Score 600.5; DB 4; Best Local Similarity 38.4%; Pred. No. 1.3e-49; Matches 129; Conservative 61; Mismatches 107;
                                                                                                                                                                                                                                                                                                                                            ; Sequence 10, Application US/10355975A
; Patent No. 6759223
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ORGANISM: Mus musculus
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LENGTH: 355
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US-09-733-388-2
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                                                                                                                                                                                        Length 356;
                                                                                                                                                                                       22.2%; Score 603; DB 4; Length 356 38.1%; Pred. No. 7.7e-50; vative 62; Mismatches 106; Indels
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Sequence 10, Application US/09579664B

Patent No. 65147109;
GENERAL INCORMATION:
APPLICANT: Immunex Corporation
APPLICANT: Bird, Timochy A.
APPLICANT: Martin, Unja
APPLICANT: Martin, Unja
APPLICANT: Anderson, Dirk M.
TILE OF INVENTION: NOVEL WURINE AND HUMAN KINASES
FILE REFERENCE: 2923-A
CURRENT APPLICATION NUMBER: US/09/579,664B
CURRENT FILING DATE: 2000-05-26
NUMBER OF SEQ ID NOS: 36
SOFTWARE: Patentin version 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ------DASTSSCSEILPTSAEK 513
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PRIOR FILING DATE: 2000-12-07
PRIOR APPLICATION NUMBER: US 60/169,428
PRIOR FILING DATE: 1999-12-07
NUMBER OF SEQ ID NOS: 5
SOFWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 38.4%
Matches 129; Conservative
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Best Local Similarity 38.13
Matches 128; Conservative
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CRGANISM: Mus musculus
US-09-579-6648-10
                                                                                                                                     ORGANISM: Homo sapiens
                                                                                                      LENGTH: 356
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                                                                                                                         TYPE: PRT
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                                                                             SAVDCWSLGVILFVCLCGYPPFSEQNSNIPLKNQIAEGKYTYIAAAWRNVSEQAFDLVKN
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FILING DATE:
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STATE:
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APPLICANT: Scoville, John
APPLICANT: Scoville, John
APPLICANT: Turner, C. Alexander Jr.
APPLICANT: Turner, C. Alexander Jr.
APPLICANT: Zambrowicz, Brian
APPLICANT: Zambrowicz, Brian
APPLICANT: Sands, Arthur T.
TITLE OF INVENTION: No. 6806073el Human Kinase Proteins and
TITLE OF INVENTION: Polynucleotides Encoding the Same
FILE REPERRENCE: LEX-0103-USA
CURRENT APPLICATION NUMBER: US/10/446,175
CURRENT FILING DATE: 2003-05-27
PRIOR APPLICATION NUMBER: US/09/733,388
PRIOR PILING DATE: 2000-12-07
PRIOR PILING DATE: 2000-12-07
PRIOR FILING DATE: 1999-12-07
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 22.1%; Score 600.5; DB 4; Length 385; Best Local Similarity 38.4%; Pred. No. 1.5e-49; Matches 129; Conservative 61; Mismatches 107; Indels 39
APPLICANT: Donoho, Greg
APPLICANT: Scoville, John
APPLICANT: Turner, C. Alexander Jr.
APPLICANT: Turner, C. Alexander Jr.
APPLICANT: Friedrich, Glenn
APPLICANT: Abuin, Alejandro
APPLICANT: Samds, Arthur T.
TITLE OF INVENTION: Polynucleotides Encoding the Same
FILE REFERENCE: LEX-0103-USA
CURRENT APPLICANT: APPLICANTION NUMBER: US/09/733,388
CURRENT APPLICANTON NUMBER: US/09/733,388
CURRENT FILING DATE: 1999-12-07
PRIOR APPLICATION NUMBER: US 60/169,428
PRIOR APPLICATION NUMBER: US 60/169,428
PRIOR FILING DATE: 1999-12-07
NUMBER OF SEQ ID NOS: 5
SOFTWARE: FRSEEQ FOR WINDOWS Version 4.0
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Patent No. 6806073
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                    ) ORGANISM: Homo sapiens
US-09-733-388-2
                                                                                                                                                                                                                                                                                                                           SEQ ID NO 2
LENGTH: 385
TYPE: PRT
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                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                         39;
                                                                                                                                                                                                      22.1%; Score 600.5; DB 4; Length 38.4%; Pred. No. 1.5e-49; tive 61; Mismatches 107; Indels
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310 FNATAVVRHMRKLHLGSSLDSSNASVSSSLSLASQK 345
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FastSEQ for Windows Version 2.0
NUMBER OF SEQ ID NOS: 5
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: Incyte Pharmaceuticals, STREET: 3174 Porter Drive CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 19, Application US/08878989
Patent No. 5885803
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bandman, Olga
Hillman, Jennifer
Corley, Neil C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Guegler, Karl G.
Lal, Preeti
Goli, Surya K.
Shah, Purvi
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COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J J
                                                                                                                                                                                                      Query Match
Best Local Similarity 38.4°
Matches 129; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: FASESEQ for
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US
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PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM: MEDIUM TYPE: Diskett
                                                                          LENGTH: 385
TYPE: PRT
CRGANISM: Homo sapiens
US-10-446-175-2
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CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                 NAME: Billings, Lucy J J
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-
TELECOMMUNICATION:
TELEPHONE: 415-855-0555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INFORMATION FOR SEQ ID NO: 19:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
LENGTH: 370 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: GenBank
CLONE: 790790
US-09-272-796-19
                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: 415-845-4166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      486 IIRKRGHEWDQ 496
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I.ENGTH: 370
TYPE: PRT
; ORGANISM: Human
US-09-457-040B-31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AVQYLHENGVIHRDLKPENVLLSSTSEECCIKITDFGQSKILGETSLMRTLCGTPTYLAP 365
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          244 DISDSAKDFIRHLMEKDPEKRFTCEQALQHPWIAGDT-----ALDKNIHQSVSEQIKKN 297
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 370;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61; Mismatches 107; Indels
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APPLICANT: Hillman, Jennifer L.
APPLICANT: Corley, Neil C.
APPLICANT: Guegler, Karl G.
APPLICANT: Gali, Preeti
APPLICANT: Gali, Surya K.
APPLICANT: Shah, Purvi
APPLICANT: Shah, Purv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 591.5; DB 2
Pred. No. 1.1e-48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
COMPUTER: DISK DOS
SOFTWARE: FastSEQ for Windows Version 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STREET: 3174 Porter Drive CITY: Palo Alto
                                                    REFERENCE/DOCKET NUMBER: PF-0321 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-09-272-796-19
; Sequence 19, Application US/09272796
Patent No. 6207148
; GENERAL INFORMATION:
                           36,749
                                                                                                                                                                                                   INFORMATION FOR SEQ ID NO: 19: SEQUENCE CHARACTERISTICS: LENGTH: 370 amino acide TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                21.8%;
39.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches 124; Conservative
                                                                                                                                                                                                                                                                                             ; TYPE: amino acid
; STRANDEDESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GenBank
; CLONE: 790790
US-08-878-999-19
                                                                                                                                           TELEFAX: 415-845-4166
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                     REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Ph
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   186 KDFIDKYIMSRPIGSGACGEVKLAFQKSVCKKVAVKIISKRKFKMNTSSNEHPISVDTEI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 21.8%; Score 591.5; DB 3; Length : Best Local Similarity 39.9%; Pred. No. 1.1e-48; Matches 124; Conservative 61; Mismatches 107; Indels
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APPLICANT: Vertex Pharmaceuticals Incorporated
APPLICANT: Vertex Pharmaceuticals Incorporated
APPLICANT: Vertex Prove
TITLE OF INVENTION: Crystallized P38 Complexes
FILE REFERENCE: VPI/98-14
CURRENT APPLICATION NUMBER: US/09/457,040B
CURRENT FILING DATE: 1999-12-08
NUMBER OF SEQ ID NOS: 41
SOFTWARE: PatentIn version 3.0
                                                                                                                                                                                                          PF-0321 US
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CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/878,989
FILLING DATE:
ATTORNEY/AGENT INFORMATION:
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; TYPE: PRT
; ORGANISM: Human
US-09-949-016-7461
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                                                                                                                                 246 BILKKLDHPCIIKIENFFDSEDFYYIVLELMEGGELFDRVVNSTRLREPIAKLYFYQMLL 305
                                                                                                                                                    AVQYLHENGVIHRDLKPENVLLSSTSEECCIKITDFGQSKILGETSLMRTLCGTPTYLAP 365
                                                                                                                                                                                                                  EVLNTAGTTGYSSAVDCWSLGVILFVCLCGYPPFSEQNSNIPLKNQIAEGKYTYIAAAWR 425
                                                                                                                                                                                                                                                                                   ||---AQKPYSKAVDCWSIGVIAYILLCGYPPFYDEN-DAKLFEQILKAEYEFDSPYWD 243
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                                                                                               EDIRDIYDFRDVLGTGAFSEVILAEDKRTQKLVAIKCIAKEALEGKEGSMEN-----EI
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Sequence 1314, Application US/09538092

Patent No. 6753314

GENERAL INFORMATION:

APPLICANT: Giot, Loic

APPLICANT: Mansfield, Traci A.

TITLE OF INVENTION: Protein-Protein Complexes and Method of Using Same

TITLE OF INVENTION: 1596-542

CURRENT APPLICATION NUMBER: 60/129

PRIOR APPLICATION NUMBER: 60/129

PRIOR PILING DATE: 1999-04-01

PRIOR PILING DATE: 1999-04-01

PRIOR PILING DATE: 1999-04-01

PRIOR PILING DATE: 1399-04-01

NUMBER OF SEQ ID NOS: 1387

SOFWWARE: CuraPatSeqFormatter Version 0.9

SEQ ID NO 1314
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 21.8%; Score 591.5; DB 3; Length 39.9%; Pred. No. 1.1e-48; Live 61; Mismatches 107; Indels
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OTHER INFORMATION: Polypeptide Accession Number Q14012
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 39.9°
Matches 124, Conservative
                                  Matches 124; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                486 IIRKRGHEWDQ 496
                                                                                                                                                                                                                                                                                                                                                                                                                             298 FAKSK---WKQ 305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: misc_feature
LOCATION: (0)...(0)
Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-09-538-092-1314
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Sequence 7461, Application US/09949016

Batent No. 6812339

GENERAL INFORMATION:
PARELL SAFEMENT STATES, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-09-08
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 7461
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                                                                                                                                                         244 DISDSAKDFIRHLMEKDPEKRFTCEQALQHPWIAGDT----ALDKNIHOSVSEQIKKN 297
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EVLNTAGTTGYSSAVDCWSLGVILFVCLCGYPPFSEQNSNIPLKNQIAEGKYTYIAAAWR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     426 NVSEQAFDLVKNLLVVDPEQRLTTKQALEHPWLQDDSMKHTVERLMYGVDHTMPPPIKKN
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298 FAKSK---WKQ 305
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